

SEARCH REQUEST FORM

111215

Requestor's Name: _____ Serial Number: _____
Date: _____ Phone: _____ Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

STAFF USE ONLY

Date completed: 12/31/83
Searcher: [Signature]
Terminal time: _____
Elapsed time: 15 min
CPU time: _____
Total time: _____
Number of Searches: _____
Number of Databases: _____

Search Site

____ STIC
____ ☒ CM-1
____ Pre-S

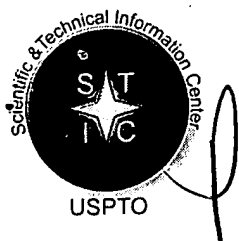
Type of Search

____ N.A. Sequence
____ ☒ A.A. Sequence
____ Structure
____ Bibliographic

Vendors

____ IG
____ STN
____ Dialog
____ APS
____ Geninfo
____ SDC
____ DARC/Questel
____ ☒ Other

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STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 111215

TO: Phillip Gambel
Location: 8b03 / 9e12
Wednesday, December 31, 2003
Art Unit: 1644
Phone: 308-3997
Serial Number: 09 / 917410

From: Jan Delaval
Location: Biotech-Chem Library
Remsen Building
E01 - A51
Phone: 571-272-2504
jan.delaval@uspto.gov

Search Notes

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011215

Delavai, Jan

From: Gambel, Phillip
Sent: Wednesday, December 31, 2003 10:29 AM
To: Delavai, Jan
Subject: 09 / 917,410 multiple organ failure amd

jan

please perform a sequence and a sequence interference search for

09/ 917,410 multiple organ failure amd

SEQ ID NO: 2

SEQ ID NO: 4

SEQ ID NO: 5

SEQ ID NO: 6

thanx

phillip gambel
art unit 1644
308-3997

1644 mailbox 9e12

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 31, 2003, 10:29:11 ; Search time 8.36569 Seconds

(Without alignments)
2506.043 Million cell updates/sec

Title: US-09-917-410-2

Sequence: 1 DIOMTQSPSLASVGDRTV.....EVTHTGSLSPVTKSFNRGEC 218

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 76:*
2: PIR1:*
3: PIR2:*
4: PIR3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	952.5	83.8	215	2 JE0242	Ig kappa chain NIG
2	919.5	80.9	215	2 JE0244	Ig kappa chain NIG
3	897.5	78.9	215	2 JE0243	Ig kappa chain NIG
4	878.5	77.3	215	2 A23746	Ig kappa chain V-I
5	872	76.7	216	2 JE0241	Ig kappa chain Am3
6	757	66.6	240	2 S06084	Ig kappa chain pre
7	740	65.1	218	2 S68241	Ig kappa chain V r
8	738	64.9	218	2 JC5810	Ig kappa chain V r
9	725	63.8	234	2 S14237	Ig kappa chain pre
10	724	63.7	230	2 S33151	Ig kappa chain pre
11	723	63.6	210	2 A56169	Ig kappa chain V r
12	722	63.5	220	2 A31790	Ig kappa chain V r
13	716.5	63.0	219	2 S38865	Ig kappa chain - m
14	713	62.7	234	2 S01320	Ig kappa chain pre
15	700.5	61.6	219	2 S52028	Ig kappa chain (mo
16	697.5	61.3	214	2 S68212	Ig kappa chain - m
17	695.5	61.2	217	2 S42772	Ig kappa chain (Ma
18	692.5	60.9	225	2 S37484	Ig kappa chain - m
19	688.5	60.6	225	2 J10029	Ig kappa chain pre
20	688.5	60.6	225	2 S25058	Ig kappa chain pre
21	688.5	60.5	219	2 S16112	Ig kappa chain V r
22	687.5	60.5	215	2 S52029	Ig kappa chain V r
23	620.5	54.7	135	2 S70219	Ig kappa chain V-C
24	599	52.6	178	2 A20969	Ig kappa chain pre
25	568.5	50.0	229	1 K3HU	Ig kappa chain C r
26	548	48.2	106	1 K3HU	Ig kappa chain C r
27	539.5	47.4	238	2 A49633	Ig kappa chain (Ma
28	537.5	47.3	197	2 S29583	Ig kappa chain (Ma
29	513	45.1	99	2 A37927	Ig kappa chain C r

30	512	45.0	127	2 S40367	Ig kappa chain V-U
31	507	44.6	99	2 S26653	Ig kappa chain C r
32	499	43.9	141	2 A49134	Ig kappa chain V-I
33	491	43.2	123	2 S40331	Ig kappa chain - h
34	490	43.1	108	2 B49047	Ig kappa chain V r
35	490	43.1	233	2 S29577	Ig kappa chain - r
36	489	43.0	109	2 S31988	Ig kappa chain - h
37	486	42.7	111	1 KVM508	Ig kappa chain V r
38	485	42.7	108	2 S44122	Ig kappa chain V r
39	485	42.7	139	2 S40365	Ig kappa chain - h
40	483	42.5	111	1 KVM569	Ig kappa chain V r
41	482	42.4	144	2 P10106	Ig kappa chain pre
42	480	42.2	111	1 KVM543	Ig kappa chain V r
43	480	42.2	125	2 S40333	Ig kappa chain V r
44	478	42.0	130	2 S40368	Ig kappa chain - h
45	474	41.7	111	1 KVM583	Ig kappa chain V r

ALIGNMENTS

RESULT 1

JE0242

Ig kappa chain NIG26 precursor - human

C/Species: Homo sapiens (man)

C/Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #ext_change 21-Jan-2000

C/Accession: JE0242

R/Alim: M.A.; Yamaki, S.; Hosain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda,

submitted to JIPID, November 1998

A/Description: Structure relationship of kappa type light chains with AL amyloidosis: Mu

A/Reference number: JE0241

A/Accession: JE0242

A/Molecule type: protein

A/Residues: 1-215 <ALI>

C/Superfamily: immunoglobulin V region; immunoglobulin homology

F/16-91/Domain: immunoglobulin homology <IMM>

Query Match 83.8%; Score 952.5; DB 2; Length 215;

Best Local Similarity 83.5%; Pred. No. 7.4e-55;

Matches 182; Conservative 15; Mismatches 18; Indels 3; Gaps 1;

QY	1	DIOMTQSPSLASVGDRTVITTTKASQSVDDSDSTMMNYYQKPGAPKILLIYAASNTLS	60
DB	1	EIVLTQSPGTLISPERATLSCRASQSV---SNNYLAWYQKPGAPSLIIDAASRRAT	57
QY	61	GIPSRFGSGSGDTFTLTSSLOPEPFAHYCCQSQSDEDPWTFGQTKVEIKRTVAAPSVF	120
DB	58	GIDRFRSGSGSGDTFTLTSSLOPEPFAHYCCQSQSDEDPWTFGQTKVEIKRTVAAPSVF	117
QY	121	IFPPSDQLKSGTASVAVCLNNFYPREAKVQWVDNALQSGNSQESVTEQDSKDSTYSLS	180
DB	118	IFPPSDQLKSGTASVAVCLNNFYPREAKVQWVDNALQSGNSQESVTEQDSKDSTYSLS	177
QY	181	STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	218
DB	178	STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	215

RESULT 2

JE0244

Ig kappa chain NIG2 precursor - human

C/Species: Homo sapiens (man)

C/Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #ext_change 21-Jan-2000

C/Accession: JE0244

R/Alim: M.A.; Hara, Y.; Hosain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.;

submitted to JIPID, November 1998

A/Description: A new subgroup of k type light chains (VKV) identified in cases of AL am

A/Reference number: JE0243

A/Accession: JE0244

A/Molecule type: protein

A/Residues: 1-215 <ALI>

C/Superfamily: immunoglobulin V region; immunoglobulin homology

F/16-90/Domain: immunoglobulin homology <IMM>

[illegible]

```

RESULT 3
JB0243
Ig kappa chain NIG93 precursor - human
C/Species: Homo sapiens (man)
C/Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C/Accession: JB0243
R:Alt, M.A.; Hara, Y.; Hossein, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazii, H.;
submitted to JEPID, November 1998
A/Description: A new subgroup of k type light chains (YKV) identified in cases of AL amyloidosis
A/Reference number: JB0243
A/Accession: JB0243
A/Molecule type: protein
A/Residues: 1-215 <Alt>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
#16-90/Domain: immunoglobulin homology <IMM>

```

	Query Match	78.9%	Score 897.5	DB 2	Length 215
	Best Local Similarity	81.3%	Pred. No. 2.6e-51		
	Matches 178	Conservative 16	Mismatches 20	Indels 5	Gaps 2
QY	1	DIOMTQSSPSLSASVGDRTVITICKASQSVVDGDSYMNMYOQPKPAKPLIYAASNTES	60		
DB	1	EIVMTQSPATLSVSGERATLSCRASQSV---ATNVVVMYMKLQAAPRLIYDASTRAT	56		
QY	61	GIPSPFSGSGSTDTLTITSLQPEDPATYVCOQSNEDPWFEGSGTKYEIK-RTAAPS	119		
DB	57	GVPAPFSGSGSTETLTITSLQSEDFALTYQOHNNAMPPTFGGQTKETKRTIYAASV	116		
QY	120	FIFPSPDEOLKSGTASVCLNNFFYPRAKQVMKYDNALQSGNSQESVTEQDSKDYSL	179		
DB	117	FIFPSPDEQLKSGTASVCLNNFFYPRAKQVMKYDNALQSGNSQESVTEQDSKDYSL	176		
QY	160	SSTLTLSKADIEKAKYVACEVTHQGISPVYTSFPRGEC	218		
DB	177	SSTLTLSKADYEKAKYVACEVTHQGISPVYTSFPRGEC	215		

```

RESULT 4
A33746
is kappa chain V-II (KAU cold agglutinin) - human
CSpecies: Homo sapiens (man)
CDate: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
CAccession: A23746
RLeoni, J.; Ghiso, J.; Frangione, B.
J. Biol. Chem. 266, 2836-2842, 1991
A>Title: The primary structure of the Fab fragment of protein KAU, a monoclonal
A.Reference number: A23746; MUID:91131575; PMID:193660
A.Accession: A23746
A>Status: preliminary
A.Molecule type: protein
A.Residues: 1-215 <LEO>

```

C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;15-91/Domain: immunoglobulin homology <IMM>

	Query Match	77.3% Best Local Similarity	Score 878.5 11.1%	DB 2 Pred. 0.45e-50	Length 215 Matches 176	Mismatches 14	Indels 3	Gaps 1
Qy	1	DIQNTGSPSSLSASVGDRAVTITTCASQSVYDGDSTYNNWTQQRKPKPKLLIYAASLES	60					
Db	1	EIVLTQSPATLSLSPGERATLISGASQSV--SSNYLAWYQQRKGQAPRLIYDASSRAT	57					
Qy	61	GIPERFEGSGSGDFTLTISLSLOPEDPATYCCQSQSNEDEPMTFGCGTKVELIKRTVAASVF	120					
Db	58	GIPERFEGSGSGDFTLTISLSLEPEDPAVYVYGGQYGSPLTFGGGTIVELIKRTVAASVF	117					
Qy	121	IFPSPDSQLKSGTASVVCCLNNFYPREAKYQWKVDNALQSGNSQESVTEEDS KDSITYSLS	180					
Db	118	IFPSPDSQLKSGTASVVGCLNNFPPRAKAYQWKVDNALQSGNSQESVTEEDSKDSITYSLS	177					
Qy	181	STLTLSKADYEKHYVAACEVTHQGLSPVTKSPFRGE	217					
Db	178	STLTLSKADYEKHYVAACEVTHQGLSPVTKSPFRGE	214					

```

RESULT 5
JE0241
Ig kappa chain Am37 precursor - human
C|Species: Homo sapiens (man)
C|Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C|Accession: JE0241
R|Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda,
submitted to JIPIID, November 1998
A|Description: Structure relationship of kappa2type light chains with AL amyloidosis: Mu
A|Reference number: JE0241
A|Accession: JE0241
A|Molecule type: protein
A|Residues: 1-216 <Alt>
C|Superfamily: Immunoglobulin V region, immunoglobulin homology
F|16-92|Domain: Immunoglobulin homology <IIm>

```

[illegible]

RESULT 6
S06084
Ig kappa chain precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 28-Feb-1990 #sequence _revision 28-Feb-1990 #text_change 21-Jan-2000
C:Accession: S06084
R:Crowe, J.S.; Smith, M.A.; Cooper, H.J.
Nucleic Acids Res. 17, 7992, 1989
A:Title: Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain cDNA
A:Reference number: S06084; MUID:90016888; PMID:2508667
A:Accession: S06084

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OM protein - protein search, using sw model

Run on: December 31, 2003, 10:29:10 ; Search time 5.24906 Seconds

(without alignments)
1953.078 Million cell updates/sec

Title: US-09-917-410-2

Perfect score: 1137
Sequence: 1 DIQMTGSPSSLSASVGDRT.....EVTHGSLSPVTSFNRGEC 218

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	548	48.2	106	1 KAC_HUMAN	P01834 homo sapien
2	486	42.7	111	1 KV3Q_MOUSE	P01667 mus musculu
3	483	42.5	111	1 KV3Q_MOUSE	P01669 mus musculu
4	480	42.2	111	1 KV3M_MOUSE	P01665 mus musculu
5	474	41.7	111	1 KV3N_MOUSE	P01666 mus musculu
6	469	41.2	108	1 KV1B_HUMAN	P01594 homo sapien
7	469	41.2	108	1 KV1H_HUMAN	P01600 homo sapien
8	465.5	40.9	110	1 KV3P_MOUSE	P01668 mus musculu
9	465	40.9	111	1 KV3L_MOUSE	P01664 mus musculu
10	456	40.1	108	1 KV1E_HUMAN	P01597 homo sapien
11	456	40.1	108	1 KV1M_HUMAN	P01605 homo sapien
12	456	40.1	129	1 KV1G_HUMAN	P04431 homo sapien
13	453	39.8	108	1 KV1W_HUMAN	P01599 homo sapien
14	453	39.8	108	1 KV1N_HUMAN	P01606 homo sapien
15	452	39.8	108	1 KV1R_HUMAN	P01610 homo sapien
16	450	39.6	108	1 KV1V_HUMAN	P04430 homo sapien
17	449	39.5	108	1 KV1F_HUMAN	P01598 homo sapien
18	449	39.5	108	1 KV1X_HUMAN	P01603 homo sapien
19	448	39.4	108	1 KV1O_HUMAN	P01604 homo sapien
20	443	39.0	108	1 KV1P_HUMAN	P01608 homo sapien
21	442	38.9	108	1 KV1A_HUMAN	P01593 homo sapien
22	439	38.6	108	1 KV1Y_HUMAN	P01611 homo sapien
23	438	38.5	108	1 KV1S_HUMAN	P01611 homo sapien
24	435	38.3	108	1 KV1L_HUMAN	P01660 mus musculu
25	433	38.1	111	1 KV3H_MOUSE	P01596 homo sapien
26	432.5	38.0	107	1 KV1T_HUMAN	P01612 homo sapien
27	431.5	38.0	109	1 KV1I_HUMAN	P01661 mus musculu
28	431	37.9	131	1 KV3I_MOUSE	P01609 homo sapien
29	429	37.7	108	1 KV1Q_HUMAN	P01595 homo sapien
30	424	37.3	108	1 KV1C_HUMAN	P01662 mus musculu
31	422	37.1	111	1 KV3J_MOUSE	P06314 homo sapien
32	422	37.1	134	1 KV4C_HUMAN	P01659 mus musculu
33	420	36.9	112	1 KV3G_MOUSE	P01659 mus musculu

34	420	36.9	129	1 KV1X_HUMAN	P04432 homo sapien
35	420	36.9	132	1 KV3F_MOUSE	P01658 mus musculu
36	417	36.7	111	1 KV3K_MOUSE	P01663 mus musculu
37	416	36.6	112	1 KV1U_HUMAN	P01613 homo sapien
38	409.5	36.0	129	1 KV3M_HUMAN	P01665 homo sapien
39	408	35.9	114	1 KV4A_HUMAN	P01602 homo sapien
40	408	35.9	117	1 KV1D_HUMAN	P01656 mus musculu
41	405	35.6	111	1 KV3C_MOUSE	P01670 mus musculu
42	405	35.6	111	1 KV3S_MOUSE	P01671 mus musculu
43	405	35.6	111	1 KV3R_MOUSE	P01654 mus musculu
44	402	35.4	111	1 KV3A_MOUSE	P01601 homo sapien
45	402	35.4	117	1 KV1I_HUMAN	

ALIGNMENTS

RESULT 1
KAC_HUMAN STANDARD; PRT; 106 AA.
ID KAC_HUMAN
AC P01834;
DT 21-JUL-1986 (Ref. 01, Created)
DT 21-JUL-1986 (Ref. 01, Last sequence update)
DT 15-SEP-2003 (Ref. 42, Last annotation update)
DE 19 kappa chain C region.
GN IGKC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE (MYELOMA PROTEIN EU).
RX MEDLINE=71064023; PubMed=5489770;
RA Gottleib P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VI. Amino acid sequence of the light chain.";
RL Biochemistry 9:3155-3161 (1970).
RN [2]
RP DISULFIDE BONDS.
RX MEDLINE=71064027; PubMed=4923144;
RA Gall W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X. Intrachain disulfide bonds.";
RL Biochemistry 9:3188-3196 (1970).
RN [3]
RP SEQUENCE (BENCE-JONES PROTEIN TI).
RX MEDLINE=72188439; PubMed=5027703;
RA Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein TI). IV. The complete amino acid sequence and its significance for the mechanism of antibody production.";
RL Hoppe-Seyler's Z. Physiol. Chem. 353:189-208 (1972).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=81042304; PubMed=675818;
RA Hietzer P.A., Max E.E., Seidman J.G., Maizel J.V. Jr., Leder P.;
RT "Cloned human and mouse kappa immunoglobulin constant and J region genes conserve homology in functional segments.";
RL Cell 22:197-207 (1980).
RN [5]
RP SEQUENCE (BENCE-JONES PROTEIN ROY).
RA Hilschmann N., Barnikol H.U., Hees M., Langer B., Ponertingl H., Steinmetz-Kayne M., Suter L., Watanabe S.;
RL (In) Franek F., Shugar D. (eds.);
RL Gamma globulins: structure and function, pp.57-74, Academic Press, New York (1969).
RN [6]
RP SEQUENCE (BENCE-JONES PROTEIN CUM).
RX MEDLINE=68242259; PubMed=5586923;
RA Hilschmann N.;
RT "The complete amino acid sequence of Bence Jones protein Cum (kappa-type).";

RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
 RN [7]
 RP SEQUENCE (BENCE-JONES PROTEIN AG).
 RX MEDLINE=69234734; PubMed=4893682;
 RA Titant K., Shinoda T., Putnam F.W.;
 RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
 RL complete sequence and the location of the disulfide bridges";
 RN J. Biol. Chem. 244:3550-3560(1969).
 RN [8]
 RP SEQUENCE (WALDENSTROM'S MACROGLOBULIN OU).
 RX MEDLINE=70201507; PubMed=5447531;
 RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
 RT "Macroglobulin structure: variable sequence of light and heavy
 RL chains";
 RN Science 169:56-59(1970).
 RN [9]
 RP SEQUENCE OF 1-33; 38-41 AND 62-80.
 RX TISSUE=Abdominal adipose tissue;
 RN PubMed=9588180;
 RX Olsen K.E., Sletten K., Westermarck P.;
 RT "Extended analysis of Al-amyloid protein from abdominal wall
 RL subcutaneous fat biopsy: kappa IV immunoglobulin light chain.";
 CC Biochem. Biophys. Res. Commun. 245:723-726(1998)
 CC -1- MISCELLANEOUS: THE EU SEQUENCE HAS THE INV (3) ALLOTYPIC MARKER,
 CC 45-ALA & 83-VAL. THE ROY SEQUENCE HAS THE INV (1,2) ALLOTYPIC
 CC MARKER, 45-ALA AND 83-LEU.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -----
 DR EMBL: J00241; AAA58989.1; -
 DR EMBL: V00557; CAA23823.1; -
 DR PIR: B90562; K3HU.
 DR PDB: 1D5B; 09-FEB-00.
 DR PDB: 1D51; 09-FEB-00.
 DR PDB: 1D6V; 04-OCT-00.
 DR PDB: 1HEZ; 10-AUG-01.
 DR PDB: 1HKL; 12-MAR-97.
 DR PDB: 117Z; 08-AUG-01.
 DR PDB: 1M1M; 15-MAY-97.
 DR Genew; HGNC:5716; IGKC.
 DR MIM; 147200; -
 DR GO; GO:0003823; P:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG cl.
 DR InterPro; IPR003006; IG_MHC.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00407; Igcl; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region; 3D-structure.
 FT NON TER 1 1
 FT DOMAIN 5 102 IG-LIKE.
 FT DISULFID 26 86
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
 FT VARIANT 83 83 V -> L (IN INV(1,2) MARKER).
 FT /FTID=VAR_003897.
 FT CONFLICT 14 14 D -> N (IN REF. 7 AND 8).
 FT CONFLICT 57 57 E -> Q (IN REF. 5 AND 6).
 SQ SEQUENCE 106 AA; 11609 MW; 51984D1FD372CE8 CRC64;
 Query Match 48.2%; Score 548; DB 1; Length 106;
 Best Local Similarity 100.0%; Pred. No. 2; 8e-38;
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 TVAAPSVFI PPSEDEQLKSGTASVCLNNFYPRKAVQWKVDNALQSGNSQESVTEQDS 172

DB 1 TVAAPSVFI PPSEDEQLKSGTASVCLNNFYPRKAVQWKVDNALQSGNSQESVTEQDS 60
 QY 173 KDSYLSSTLTLSKADYEKHKVYACEVTHQGLSPYTKSNRREC 218
 DB 61 KDSYLSSTLTLSKADYEKHKVYACEVTHQGLSPYTKSNRREC 106
 RESULT 2
 KV30_MOUSE STANDARD; PRT; 111 AA.
 ID KV30_MOUSE
 AC P01667;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-II region PC 6308.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxId=10090;
 RX MEDLINE=79073152; PubMed=103003;
 RA Weigert M., Gattaman L., Loh B., Schilling J., Hood L.E.;
 RT "Rearrangement of genetic information may produce immunoglobulin
 RL diversity";
 DR Nature 276:785-790(1978).
 DR PIR: C01937; KMS08.
 DR HSSP; P80362; 1WTL.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 39 53 FRAMEWORK-2.
 FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 61 92 FRAMEWORK-3.
 FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.
 FT DISULFID 102 111 FRAMEWORK-4.
 FT NON TER 111 111 BY SIMILARITY.
 SQ SEQUENCE 111 AA; 12071 MW; 7A4ADE4D6C256D29 CRC64;
 Query Match 42.7%; Score 486; DB 1; Length 111;
 Best Local Similarity 80.2%; Pred. No. 3; 4e-33;
 Matches 89; Conservative 10; Mismatches 12; Indels 0; Gaps 0;
 QY 1 DIOMTQSPSSLSASVGRVTITCKRASQSVDPDGSYMMWYQKDGKAPKLIYASNLDS 60
 DB 1 DIVLTQSPASLAIVSGQATISCKRSGSVDPDGSYMMWYQKDGKAPKLIYASNLDS 60
 QY 61 GIPSRFSGSGGTDTFTLTSLQPEDEFAITYYCOGSNEDPMTFGGTQKYEIK 111
 DB 61 GIPARFSGSGGTDTFTLTSLQPEDEFAITYYCOGSNEDPMTFGGTQKYEIK 111
 RESULT 3
 KV30_MOUSE STANDARD; PRT; 111 AA.
 ID KV30_MOUSE
 AC P01669;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-II region PC 7769.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxId=10090;
 RX [1]

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 31, 2003, 10:29:10 ; Search time 18.5357 Seconds

(without alignments)
3034.973 Million cell updates/sec

Title: US-09-917-410-2

Perfect score: 1137
Sequence: 1 DIQMTGSPSSLSASVGDRT.....ETHHGUSLSPVTSFNRGEC 218

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL_23:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phase:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriophage:*

17: sp_archaeop:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES:

Result No.	Score	Query Match	Length	DB ID	Description
1	929	81.7	234	4	Q8NEK1
2	899.5	79.1	239	4	Q8TCD0
3	898.5	79.0	239	4	Q8NEK0
4	747	65.7	233	11	Q91WS9
5	744	65.4	234	11	Q8R062
6	737	64.8	234	11	Q91WF8
7	733	64.5	214	11	Q91A5
8	726	63.9	234	11	Q8VCP0
9	707.5	62.2	238	11	Q9PM37
10	701.5	61.7	238	11	Q8VC16
11	701.5	61.7	239	11	Q8VC55
12	685.5	60.3	235	11	Q91W12
13	683.5	60.1	239	11	Q8K0F8
14	664	58.4	234	11	Q8R028
15	494	43.4	108	4	Q9U177
16	472.5	41.6	107	4	Q96SA9

17	451.5	39.7	233	4	Q8TBC9	Q8TBC9 homo sapien
18	451	39.7	108	4	Q9UL70	Q9UL70 homo sapien
19	447.5	39.4	107	4	Q9UL81	Q9UL81 homo sapien
20	446	39.2	116	4	Q96EP6	Q96EP6 homo sapien
21	445.5	39.2	237	4	Q8WTR6	Q8WTR6 homo sapien
22	443	39.0	236	4	Q8NEJ1	Q8NEJ1 homo sapien
23	442.5	38.9	237	4	Q8WUK4	Q8WUK4 homo sapien
24	431	37.9	108	4	Q9UL79	Q9UL79 homo sapien
25	425.5	37.4	233	4	Q8N5F4	Q8N5F4 homo sapien
26	425	37.4	234	4	Q8N355	Q8N355 homo sapien
27	410	36.1	111	11	Q92OE9	Q92OE9 mus musculus
28	408.5	35.9	236	4	Q96E61	Q96E61 mus musculus
29	404	35.5	240	4	Q8WUK3	Q8WUK3 mus musculus
30	396.5	34.9	235	11	Q9PM11	Q9PM11 mus musculus
31	388	34.1	109	11	Q92OE6	Q92OE6 mus musculus
32	387.5	34.1	109	4	Q9UL78	Q9UL78 mus musculus
33	385.5	33.9	112	11	Q8K1F2	Q8K1F2 mus musculus
34	383.5	33.7	112	11	Q8K1F3	Q8K1F3 mus musculus
35	382.5	33.6	114	11	Q8K1F1	Q8K1F1 mus musculus
36	382	33.6	108	4	Q9UL83	Q9UL83 mus musculus
37	380	33.4	238	11	Q9QYF0	Q9QYF0 mus musculus
38	379	33.3	103	11	Q9UL80	Q9UL80 mus musculus
39	378.5	33.3	134	11	Q8VDD0	Q8VDD0 mus musculus
40	370	32.5	107	11	Q9JL84	Q9JL84 mus musculus
41	369.5	32.5	109	4	Q9UL85	Q9UL85 mus musculus
42	368.5	32.4	109	4	Q9UL86	Q9UL86 mus musculus
43	368	32.4	108	11	Q8VJ70	Q8VJ70 mus musculus
44	363.5	32.0	233	4	Q96I69	Q96I69 mus musculus
45	360	31.7	114	4	Q9UL80	Q9UL80 homo sapien

ALIGNMENTS

RESULT 1

Q8NEK1 PRELIMINARY; PRT; 234 AA.

AC Q8NEK1;
DT 01-OCR-2002 (TEMBLrel. 22, Created)
DT 01-OCR-2002 (TEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC030813; AA030813.1; -
DR InterPro; IPR007110; IG_1ike.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGy; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25530 MW; 631E8DEBFD132F8 CRC64;

Query Match 81.7%; Score 929; DB 4; Length 234;
Best Local Similarity 82.1%; Pred. No. 1e-73;

Matches 179; Conservative 19; Mismatches 16; Indels 4; Gaps 1;

Qy 1 DIQMTGSPSSLSASVGDRTITCKASQSYDSDSYNNYQKRGKAPKLLIYAASNL65 60
Db 21 EIMTQSPATLSVSPERATLSCRASQSV---TSNLAWQGFPGSPRIVITGASRRAS 76
Qy 61 GIPSRFGSGSGTDFLTITISLOPEDFATYYCCQSNEDPWTFGQGTKEIKRTVAAPSV 120

```

Db      77  GVPAPFSGSGSGTFFLTITSLQSEDFAVVYCOQYNKMPHFQGTCKIDIKRTVAAPSVF 136
Qy      121  IFPPDEQLKSGTASVVCILNNFYREAKVQKVNALQSGNSQSESVTEODSKDSTYSL 180
Db      137  IFPPDEQLKSGTASVVCILNNFYREAKVQKVNALQSGNSQSESVTEODSKDSTYSL 196
Qy      181  STLTLSKADYEKHKYVACEVTHQGLSSPVTKSFNRGEC 218
Db      197  STLTLSKADYEKHKYVACEVTHQGLSSPVTKSFNRGEC 234

```

RESULT 2

```

O8TCD0  PRELIMINARY; PRT; 239 AA.
AC  O8TCD0;
DT  01-JUN-2002 (TREMBLrel. 21, Created)
DT  01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DE  Hypoetical protein.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxId=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  Tissue=lung;
RA  Strausberg R.;
RL  Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR  EMBL; BC022362; AAH22362.1; -.
DR  InterPro; IPR007110; IG_1like.
DR  InterPro; IPR003006; IG_MHC.
DR  InterPro; IPR003596; IG_v.
DR  Pfam; PF00047; Ig; 2.
DR  SMART; SM00406; Igv; 1.
DR  PROSITE; PS50835; IG_LIKE; 2.
DR  PROSITE; PS00290; IG_MHC; 1.
KM  Hypoetical protein.
SQ  SEQUENCE 239 AA; 26234 MW; FACEDCA3B0871D CRC64;

```

Query Match 79.1%; Score 899.5; DB 4; Length 239;
 Best Local Similarity 77.2%; Pred. No. 4,1e-71;
 Matches 169; Conservative 24; Mismatches 25; Indels 1; Gaps 1;

```

Qy      1  DIQMTQSPSSLSASVGDRVTITCKASQSVY-DGDSYMNWYQOKPKLIIYAASNLE 59
Db      21  DVMTQSPSLPVTIGQPAISICRSTQSLVSDGNTYLNWFOQRFQSGPRRLIYKVSNRD 80
Qy      60  SGIPRFGSGSGGTDFTLTISLQPEDPATYVYCOQSNEDPMTFGQGTKEIKRTVAAPSV 119
Db      81  SGVPRFRFGSGSGGTDFTLTITRVEADVGVVFCMGQTHMPSIFFGQGTLEIKRTVAAPSV 140
Qy      120  FIFPPSDEQLKSGTASVVCILNNFYPREAKVQKVNALQSGNSQSESVTEODSKDSTYSL 179
Db      141  FIFPPSDQLKSGTASVVCILNNFYPREAKVQKVNALQSGNSQSESVTEODSKDSTYSL 200
Qy      180  SFTLTLSKADYEKHKYVACEVTHQGLSSPVTKSFNRGEC 218
Db      201  SFTLTLSKADYEKHKYVACEVTHQGLSSPVTKSFNRGEC 239

```

RESULT 3

```

O8NEKO  PRELIMINARY; PRT; 239 AA.
AC  O8NEKO;
DT  01-OCT-2002 (TREMBLrel. 22, Created)
DT  01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DE  Hypoetical protein.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxId=9606;

```

```

RN  [1]
RP  SEQUENCE FROM N.A.
RC  Tissue=Prostate;
RA  Strausberg R.;
RL  Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR  EMBL; BC030814; AAH30814.1; -.
DR  InterPro; IPR007110; IG_1like.
DR  InterPro; IPR003597; IG_c1.
DR  InterPro; IPR003006; IG_MHC.
DR  InterPro; IPR003596; IG_v.
DR  Pfam; PF00047; Ig; 2.
DR  SMART; SM00407; Igc1; 1.
DR  SMART; SM00406; Igv; 1.
DR  PROSITE; PS50835; IG_LIKE; 2.
DR  PROSITE; PS00290; IG_MHC; 1.
KM  Hypoetical protein.
SQ  SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552C0A CRC64;

```

Query Match 79.0%; Score 898.5; DB 4; Length 239;
 Best Local Similarity 79.0%; Pred. No. 5e-71;
 Matches 173; Conservative 18; Mismatches 27; Indels 1; Gaps 1;

```

Qy      1  DIQMTQSPSSLSASVGDRVTITCKASQSVY-DGDSYMNWYQOKPKLIIYAASNLE 59
Db      21  DVMTQSPSLPVTIGQPAISICRSTQSLVSDGNTYLNWFOQRFQSGPOLLILYGSNRA 80
Qy      60  SGIPRFGSGSGGTDFTLTISLQPEDPATYVYCOQSNEDPMTFGQGTKEIKRTVAAPSV 119
Db      81  SGVDRFRFGSGSGGTDFTLTISLQPEDPATYVYCOQSNEDPMTFGQGTKEIKRTVAAPSV 140
Qy      120  FIFPPSDEQLKSGTASVVCILNNFYPREAKVQKVNALQSGNSQSESVTEODSKDSTYSL 179
Db      141  FIFPPSDEQLKSGTASVVCILNNFYPREAKVQKVNALQSGNSQSESVTEODSKDSTYSL 200
Qy      180  SFTLTLSKADYEKHKYVACEVTHQGLSSPVTKSFNRGEC 218
Db      201  SFTLTLSKADYEKHKYVACEVTHQGLSSPVTKSFNRGEC 239

```

RESULT 4

```

O91WS9  PRELIMINARY; PRT; 233 AA.
AC  O91WS9;
DT  01-DEC-2001 (TREMBLrel. 19, Created)
DT  01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE  Hypoetical 25.8 kDa protein (Fragment).
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxId=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  Tissue=Colon;
RA  Strausberg R.;
RL  Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR  EMBL; BC013496; AAH13496.1; -.
DR  InterPro; IPR007110; IG_1like.
DR  InterPro; IPR003006; IG_MHC.
DR  InterPro; IPR003596; IG_v.
DR  Pfam; PF00047; Ig; 2.
DR  SMART; SM00406; Igv; 1.
DR  PROSITE; PS50835; IG_LIKE; 2.
DR  PROSITE; PS00290; IG_MHC; 1.
KM  Hypoetical protein.
FT  NON_TER
SQ  SEQUENCE 233 AA; 25781 MW; B1C184DA149A16EB CRC64;

```

Query Match 65.7%; Score 747; DB 11; Length 233;
 Best Local Similarity 64.7%; Pred. No. 9,8e-58;
 Matches 141; Conservative 28; Mismatches 45; Indels 4; Gaps 1;

```

Qy      1  DIQMTQSPSSLSASVGDRVTITCKASQSVY-DGDSYMNWYQOKPKLIIYAASNLE 60

```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 31, 2003, 10:33:16, Search time 22.4725 Seconds

(without alignments)
1539.764 Million cell updates/sec

Title: US-09-917-410-2

Sequence: 1 D1QMTQSPSSLSASVGRVT.....EVTHQGLSPVTKSPNRGEC 218

Scoring table:

BLOSUM62

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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24: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1137	100.0	218	18	AAW13563
2	1113	97.9	238	21	AAW90932
3	1113	97.9	238	23	ABR74901
4	1112	97.8	238	21	AAW90930
5	1112	97.8	238	23	ABR74899
6	1108	97.4	218	20	AAW95658
7	1108	97.4	218	21	AAW85200
8	1108	97.4	218	22	ABR76947
9	1108	97.4	238	21	AAW90931

10	1108	97.4	238	23	ABR74900	Humanised anti-Fas
11	1101	96.8	218	14	AAK33312	Humanised Mac11 Ve
12	1085	95.4	218	20	AAW50030	Human E27 anti-IGF
13	1085	95.4	218	20	AAW95660	Mus musculus anti-
14	1085	95.4	218	20	AAW95662	Mus musculus anti-
15	1085	95.4	218	21	ABR07472	Mus musculus anti-
16	1085	95.4	218	22	ABR74211	Amino acid sequenc
17	1082	95.2	218	20	AAW95669	E27 anti-IGF antib
18	1082	95.2	218	20	AAW95664	Mus musculus anti-
19	1082	95.2	218	22	ABR47087	Mus musculus anti-
20	1082	95.2	218	22	ABR76949	Anti-IGF antibody
21	1082	95.2	218	22	ABR76951	Full length light
22	1082	95.2	218	22	ABR76953	Variable light cha
23	1082	95.2	218	22	ABR76958	Variable light cha
24	1050	92.3	238	19	AAW83034	Anti-Fas humanised
25	1050	92.3	238	21	AAW90927	Humanised anti-Fas
26	1050	92.3	238	21	AAW90927	Humanised anti-Fas
27	1050	92.3	238	23	ABR74896	Humanised HFE7A de
28	1050	92.3	238	23	ABR74892	Humanised anti-Fas
29	1045	91.9	238	19	AAW83031	Anti-Fas humanised
30	1045	91.9	238	21	AAW83032	Humanised anti-Fas
31	1045	91.9	238	21	AAW90922	Humanised anti-Fas
32	1045	91.9	238	23	ABR74891	Humanised anti-Fas
33	1045	91.9	238	23	ABR74897	Humanised anti-Fas
34	1032	90.8	214	21	AAW93735	Humanised anti-Fas
35	1032	90.8	238	19	AAW83032	The kappa chain of
36	1032	90.8	238	21	AAW83032	Anti-Fas humanised
37	1032	90.8	238	21	AAW90923	Humanised anti-Fas
38	1032	90.8	238	23	ABR74892	Humanised anti-Fas
39	1032	90.8	238	23	ABR74898	Humanised anti-Fas
40	1031	90.7	238	19	AAW83035	Humanised anti-Fas
41	1031	90.7	238	21	AAW83035	Humanised anti-Fas
42	1031	90.7	238	21	AAW90928	Humanised anti-Fas
43	1031	90.7	238	23	ABR74897	Humanised HFE7A de
44	1031	90.7	238	23	ABR74893	Humanised anti-Fas
45	1030	90.6	238	19	AAW83033	Anti-Fas humanised

ALIGNMENTS

```

RESULT 1
AAW13563 standard; Protein; 218 AA.
ID      AAW13563;
XX
AC      AAW1563;
XX
DT      03-JUN-1997 (first entry)
XX
DE      Humanised anti-L-selectin antibody HuDreg 55 light chain.
XX
KW      L-selectin; humanised antibody; HuDreg 55; acute organ damage;
KM      organ failure; poly-trauma; haemorrhagic-traumatic shock.
XX
OS      Chimeric Mus sp.;
OS      Chimeric Homo sapiens.
XX
PN      WO9706822-A1.
XX
PD      27-FEB-1997.
XX
PF      14-AUG-1996; 96WO-US13152.
XX
PR      27-DEC-1995; 95US-0578953.
PR      17-AUG-1995; 95EP-0112895.
PR      19-SEP-1995; 95EP-0114696.
XX
PA      (BOEP ) BOEHRINGER MANNHEIM GMBH.
PA      (PROT-) PROTEIN DESIGN LABS INC.
XX
PI      Co W, Haselbeck A, Martin U, Schumacher G;
XX      WFI; 1997-165036/15.
DR

```

DR N-PSDB; AAT61280.

XX Using anti-selectin antibody to prevent acute organ damage and

PT multiple organ failure - during extracorporeal circulation or

PT following polytrauma, e. g. haemorrhagic-traumatic shock

XX

PS Disclosure; Page 32-33; 52pp; English.

XX

CC Humanised anti-L-selectin antibody Hudreg 55 comprises 2 light

CC chains each having the sequence given in AAM13563 and 2 heavy chains

CC each having the sequence given in AAM13564. These are encoded by the

CC cDNA clones given in AAT61280 and AAT61281. Hudreg 55 can be used to

CC prevent multiple organ failure associated with polytrauma and for

CC the prevention of acute organ damage associated with extracorporeal

CC blood circulation. The antibody inhibits interaction between the

CC carbohydrate-recognising domain of the selectin and the

CC corresponding cell surface receptor.

XX

SQ Sequence 218 AA;

Query Match 100.0%; Score 1137; DB 18; Length 218;

Best Local Similarity 100.0%; Pred. No. 1e-57; Mismatches 0; Indels 0; Gaps 0;

Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCKASQSVYDGDSDYMNWYQKPKAKPLIYAASNLES 60

DB 1 DIQMTQSPSSLSASVGRVTITCKASQSVYDGDSDYMNWYQKPKAKPLIYAASNLES 60

QY 61 GIPSPFGSGSGGTDTLTITSLQPEDPATYTCQSNEDPWFPGGQTKYKIRTAAPSVF 120

DB 61 GIPSPFGSGSGGTDTLTITSLQPEDPATYTCQSNEDPWFPGGQTKYKIRTAAPSVF 120

QY 121 IFPPSEDLKSGTASVCLNNFYPREAKVQMKVDNALQSGNSQSVTEQDSKSTYLS 180

DB 121 IFPPSEDLKSGTASVCLNNFYPREAKVQMKVDNALQSGNSQSVTEQDSKSTYLS 180

QY 121 IFPPSEDLKSGTASVCLNNFYPREAKVQMKVDNALQSGNSQSVTEQDSKSTYLS 180

DB 121 IFPPSEDLKSGTASVCLNNFYPREAKVQMKVDNALQSGNSQSVTEQDSKSTYLS 180

QY 181 STLTLSKADYKHKYVACEVTHQGLSSPVTGSFNRGEC 218

DB 181 STLTLSKADYKHKYVACEVTHQGLSSPVTGSFNRGEC 218

RESULT 2

AAM90932

ID AAM90932 standard; Protein; 238 AA.

XX

AC AAM90932;

XX

DT 08-AUG-2000 (first entry)

XX

DE Humanised anti-Fas designed light chain Leu 3 protein.

XX

XX

KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;

KW anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiac;

KW dermatological; immunosuppressive; thyromimetic; antineuritic; anti-Fas;

KW nephrotoxic; antifertility; neuroprotective; antileukemic; antileukemic;

KW hepatocarcinoma; humanized; apoptosis; systemic lupus erythematosus;

KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;

KW Sjogren's syndrome; anemia; Addison's disease; scleroderma; sterility;

KW Goodpasture syndrome; Crohn's disease; myasthenia gravis;

KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;

KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;

KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.

XX

OS Synthetic.

XX

PN EP990663-A2.

XX

PD 05-APR-2000.

XX

PF 29-SEP-1999; 99EP-0307711.

XX

XX 30-SEP-1998; 98JP-0276881.

PR 30-SEP-1998; 98JP-0276882.

XX

PA (SANY) SANKYO CO LTD.

XX

PI Serizawa N, Hanyama H, Nakahara K, Tamaki I, Takahashi T;

XX

DR WPI; 2000-258930/23.

XX

DR N-PSDB; AAT61280.

XX

PT New humanized anti-Fas antibody, useful for treating or preventing e.g.

PT inflammatory or autoimmune disease, induces apoptosis selectively in

PT cells with abnormal Fas-Fas ligand systems

XX

PS Claim 3; Page 161-162; 263pp; English.

XX

CC This invention describes a novel humanized anti-Fas antibody-like

CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas

CC ligand system, by binding to Fas on the cell surface, and prevents

CC apoptosis in cells with a normal system, by inhibiting binding between

CC Fas and its ligand. The products of the invention have anti-inflammatory,

CC anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral,

CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,

CC antineuritic, nephrotoxic, antifertility, neuroprotective,

CC antiarteriosclerotic, cardiac and hepatotropic activity. (I) induce

CC apoptosis by binding to cell surface Fas or inhibit it by competitive

CC inhibition of ligand binding. (I) are used to treat and/or prevent

CC diseases associated with the Fas/Fas ligand system, especially systemic

CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft

CC versus host disease, Sjogren's syndrome, pernicious anemia, Crohn's

CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's

CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,

CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin

CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,

CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral

CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively

CC inhibit apoptosis in normal cells but selectively induce it in abnormal

CC cells. They bind to both human and murine Fas, so can be evaluated in

CC murine disease models. (I) act on the active site of Fas, i.e. they mimic

CC the native ligand, do not induce liver disease, and have reduced risk of

CC inducing a human anti-murine antibody response. This sequence represents

CC a humanised anti-Fas antibody light chain construct designated Leu 3

CC which is described in the method of the invention.

XX

SQ Sequence 238 AA;

Query Match 97.9%; Score 1137; DB 21; Length 238;

Best Local Similarity 98.6%; Pred. No. 2.5e-56;

Matches 215; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCKASQSVYDGDSDYMNWYQKPKAKPLIYAASNLES 60

DB 21 DIQMTQSPSSLSASVGRVTITCKASQSVYDGDSDYMNWYQKPKAKPLIYAASNLES 80

QY 61 GIPSPFGSGSGGTDTLTITSLQPEDPATYTCQSNEDPWFPGGQTKYKIRTAAPSVF 120

DB 61 GIPSPFGSGSGGTDTLTITSLQPEDPATYTCQSNEDPWFPGGQTKYKIRTAAPSVF 140

QY 121 IFPPSEDLKSGTASVCLNNFYPREAKVQMKVDNALQSGNSQSVTEQDSKSTYLS 180

DB 121 IFPPSEDLKSGTASVCLNNFYPREAKVQMKVDNALQSGNSQSVTEQDSKSTYLS 200

QY 181 STLTLSKADYKHKYVACEVTHQGLSSPVTGSFNRGEC 218

DB 201 STLTLSKADYKHKYVACEVTHQGLSSPVTGSFNRGEC 238

RESULT 3

ABB74901

ID ABB74901 standard; Protein; 238 AA.

XX

AC ABB74901;

XX

DT 26-APR-2002 (first entry)

XX

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 31, 2003, 10:32:16 ; Search time 16.8954 Seconds
(without alignments)
2588.856 Million cell updates/sec

Title: US-09-917-410-2
Perfect score: 1137
Sequence: 1 D1QMTGSPSSLASVGDVRYT.....EVTHTGLISPTKSFNRGEC 218

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 733937 seqs, 200641211 residues

Total number of hits satisfying chosen parameters: 733937

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubppaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubppaa/PCTUS_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubppaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/1/pubppaa/US09C_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubppaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubppaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubppaa/US10C_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubppaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubppaa/US10C_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1137	100.0	218	9	US-09-917-410-2
2	1113	97.9	238	12	US-10-384-933-131
3	1113	97.9	238	15	US-10-216-484-131
4	1112	97.8	238	12	US-10-384-933-127
5	1112	97.8	238	15	US-10-216-484-127
6	1108	97.4	218	9	US-09-802-077-9
7	1108	97.4	218	9	US-09-802-077-9
8	1108	97.4	218	9	US-09-802-077-9
9	1108	97.4	218	9	US-09-802-077-9
10	1108	97.4	218	11	US-09-925-179-9
11	1108	97.4	218	12	US-10-113-996-13
12	1108	97.4	238	15	US-10-384-933-129
13	1108	97.4	238	15	US-10-216-484-129
14	1085	95.4	218	11	US-09-925-179-67
15	1085	95.4	218	12	US-10-292-869-1

16	1082	95.2	218	9	US-09-920-171-15	Sequence 15, Appl
17	1082	95.2	218	9	US-09-920-171-17	Sequence 17, Appl
18	1082	95.2	218	9	US-09-920-171-19	Sequence 19, Appl
19	1082	95.2	218	9	US-09-920-171-24	Sequence 24, Appl
20	1082	95.2	218	12	US-10-113-996-15	Sequence 15, Appl
21	1082	95.2	218	12	US-10-113-996-17	Sequence 17, Appl
22	1082	95.2	218	12	US-10-113-996-19	Sequence 19, Appl
23	1082	95.2	218	12	US-10-113-996-24	Sequence 24, Appl
24	1050	92.3	238	12	US-10-384-933-107	Sequence 107, App
25	1050	92.3	238	15	US-10-216-484-107	Sequence 107, App
26	1045	91.9	238	15	US-10-384-933-50	Sequence 50, Appl
27	1045	91.9	238	15	US-10-216-484-50	Sequence 50, Appl
28	1032	90.8	214	15	US-10-153-382-19	Sequence 19, Appl
29	1032	90.8	238	12	US-10-384-933-52	Sequence 52, Appl
30	1032	90.8	238	15	US-10-216-484-52	Sequence 52, Appl
31	1031	90.7	218	12	US-10-353-708-39	Sequence 39, Appl
32	1031	90.7	218	12	US-10-353-708-57	Sequence 57, Appl
33	1031	90.7	218	15	US-10-171-452A-39	Sequence 39, Appl
34	1031	90.7	218	15	US-10-171-452A-57	Sequence 57, Appl
35	1031	90.7	238	12	US-10-384-933-109	Sequence 109, App
36	1031	90.7	238	12	US-10-353-708-38	Sequence 38, Appl
37	1031	90.7	238	12	US-10-353-708-56	Sequence 56, Appl
38	1031	90.7	238	15	US-10-216-484-109	Sequence 109, App
39	1031	90.7	238	15	US-10-171-452A-38	Sequence 38, Appl
40	1031	90.7	238	15	US-10-171-452A-56	Sequence 56, Appl
41	1030	90.6	238	12	US-10-384-933-54	Sequence 54, Appl
42	1030	90.6	238	15	US-10-216-484-54	Sequence 54, Appl
43	1029	90.5	236	15	US-09-859-053-30	Sequence 30, Appl
44	1028	90.5	241	15	US-10-221-945-1	Sequence 1, Appl
45	1025	90.1	237	9	US-09-056-1608-100	Sequence 100, App

ALIGNMENTS

RESULT 1
US-09-917-410-2
Sequence 2, Application US/09917410
Patent No. US20020098183A1

GENERAL INFORMATION:
APPLICANT: MARTIN, Ulrich; HASELBECK, Anton; SCHUMACHER, Guenther;

TITLE OF INVENTION: ANTI-L-SELECTIN ANTIBODIES FOR PREVENTION OF MULTIPLE ORGAN FAILURE AFTER POLYTRAUMA AND FOR PREVENTION OF ACUTE ORGAN DAMAGE AFTER EXTRACORPOREAL BLOOD CIRCULATION

NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSSEE: Felte & Lynch

STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Computer Disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII, WordPerfect 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/917,410

FILING DATE: 26-Jul-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/576,953

FILING DATE: <Unknown>
APPLICATION NUMBER: EP 95 114 969.9

ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. US20020098183A1man D.

REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: BOER 1059-PFF/NDH/SLH
TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 218
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-917-410-2

Query Match 100.0%; Score 1137; DB 9; Length 218;
Best Local Similarity 100.0%; Pred. No. 4.5e-72;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQWTQSPSSLSASVGVDRVTITCKASQSVYDGDGSYNNWYQKPKAKPLIYAASNLES 60
DB 1 DIQWTQSPSSLSASVGVDRVTITCKASQSVYDGDGSYNNWYQKPKAKPLIYAASNLES 60
QY 61 GIPSRFSGSGSGTDFLTITSSLOPEDPATYTCQOSNEDPMTFGQGTVEIKRTVAAPSVF 120
DB 61 GIPSRFSGSGSGTDFLTITSSLOPEDPATYTCQOSNEDPMTFGQGTVEIKRTVAAPSVF 120
QY 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYSL 180
DB 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYSL 180
QY 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYSL 180
DB 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYSL 180
QY 181 STLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 218
DB 181 STLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 218

RESULT 2
US-10-384-933-131
Sequence 131, Application US/10384933
Publication No. US20030170817A1
GENERAL INFORMATION:
APPLICANT: Serizawa, No. US20030170817A1ufusa
APPLICANT: Haruyama, Hideyuki
APPLICANT: Nakahara, Kaori
APPLICANT: Takahashi, Ikuko
APPLICANT: Tamaki, Tohru
TITLE OF INVENTION: Anti-Fas Antibodies
FILE REFERENCE: 980126CIP/HG
CURRENT APPLICATION NUMBER: US/10/384,933
CURRENT FILING DATE: 2003-02-05
PRIOR APPLICATION NUMBER: US/09/499,662
PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/053,583
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 131
LENGTH: 238
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Designed light
OTHER INFORMATION: chain of humanized anti-Fas antibody
US-10-384-933-131

Query Match 97.9%; Score 1113; DB 12; Length 238;
Best Local Similarity 98.6%; Pred. No. 2.3e-70;
Matches 215; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIQWTQSPSSLSASVGVDRVTITCKASQSVYDGDGSYNNWYQKPKAKPLIYAASNLES 60
DB 1 DIQWTQSPSSLSASVGVDRVTITCKASQSVYDGDGSYNNWYQKPKAKPLIYAASNLES 60
QY 21 DIVLTQSPSSLSASVGVDRVTITCKASQSVYDGDGSYNNWYQKPKAKPLIYAASNLES 80
DB 21 DIVLTQSPSSLSASVGVDRVTITCKASQSVYDGDGSYNNWYQKPKAKPLIYAASNLES 80
QY 61 GIPSRFSGSGSGTDFLTITSSLOPEDPATYTCQOSNEDPMTFGQGTVEIKRTVAAPSVF 120
DB 61 GIPSRFSGSGSGTDFLTITSSLOPEDPATYTCQOSNEDPMTFGQGTVEIKRTVAAPSVF 120
QY 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYSL 180
DB 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYSL 180
QY 181 STLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 218
DB 181 STLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 218

QY 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYSL 180
DB 141 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYSL 200
QY 181 STLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 218
DB 201 STLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 238

RESULT 3
US-10-216-484-131
Sequence 131, Application US/10216484
Publication No. US20030103976A1
GENERAL INFORMATION:
APPLICANT: Serizawa, No. US20030103976A1ufusa
APPLICANT: Haruyama, Hideyuki
APPLICANT: Nakahara, Kaori
APPLICANT: Takahashi, Ikuko
APPLICANT: Tamaki, Tohru
TITLE OF INVENTION: Anti-Fas Antibodies
FILE REFERENCE: 980126CIP/HG
CURRENT APPLICATION NUMBER: US/10/216,484
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US/09/499,662
PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: US 09/053,583
PRIOR FILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 131
LENGTH: 238
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Designed light
OTHER INFORMATION: chain of humanized anti-Fas antibody
US-10-216-484-131

Query Match 97.9%; Score 1113; DB 15; Length 238;
Best Local Similarity 98.6%; Pred. No. 2.3e-70;
Matches 215; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIQWTQSPSSLSASVGVDRVTITCKASQSVYDGDGSYNNWYQKPKAKPLIYAASNLES 60
DB 21 DIVLTQSPSSLSASVGVDRVTITCKASQSVYDGDGSYNNWYQKPKAKPLIYAASNLES 80
QY 61 GIPSRFSGSGSGTDFLTITSSLOPEDPATYTCQOSNEDPMTFGQGTVEIKRTVAAPSVF 120
DB 61 GIPSRFSGSGSGTDFLTITSSLOPEDPATYTCQOSNEDPMTFGQGTVEIKRTVAAPSVF 140
QY 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYSL 180
DB 141 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYSL 200
QY 181 STLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 218
DB 201 STLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 238

RESULT 4
US-10-384-933-127
Sequence 127, Application US/10384933
Publication No. US20030170817A1
GENERAL INFORMATION:
APPLICANT: Serizawa, No. US20030170817A1ufusa
APPLICANT: Haruyama, Hideyuki
APPLICANT: Nakahara, Kaori
APPLICANT: Takahashi, Ikuko
APPLICANT: Tamaki, Tohru
TITLE OF INVENTION: Anti-Fas Antibodies
FILE REFERENCE: 980126CIP/HG
CURRENT APPLICATION NUMBER: US/10/384,933
CURRENT FILING DATE: 2003-02-05
PRIOR APPLICATION NUMBER: US/09/499,662

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Comugen Ltd.

OM protein - protein search, using sw model

Run on: December 31, 2003, 10:29:11 ; Search time 8.20166 Seconds

(without alignments)
1124.623 Million cell updates/sec

Title: US-09-917-410-2

Perfect score: 1137
Sequence: 1 DIQMTPSPSLASVGDRT.....ETHHGLSPRTKSPNRGEC 218

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 4231058 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA: *
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2: /cgn2_6/prodata/1/1aa/5B.COMB.pep: *
3: /cgn2_6/prodata/1/1aa/6A.COMB.pep: *
4: /cgn2_6/prodata/1/1aa/6B.COMB.pep: *
5: /cgn2_6/prodata/1/1aa/6C.COMB.pep: *
6: /cgn2_6/prodata/1/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1137	100.0	218	5 PCT-US96-13152-2	Sequence 2, Appl
2	1108	97.4	218	2 US-08-887-352B-13	Sequence 13, Appl
3	1108	97.4	218	3 US-08-466-151-9	Sequence 9, Appl
4	1108	97.4	218	3 US-09-109-207C-13	Sequence 13, Appl
5	1108	97.4	218	3 US-09-236-005-13	Sequence 13, Appl
6	1108	97.4	218	4 US-08-466-163B-9	Sequence 9, Appl
7	1085	95.4	218	3 US-09-282-505-1	Sequence 1, Appl
8	1085	95.4	218	3 US-09-054-255-1	Sequence 1, Appl
9	1085	95.4	218	4 US-09-282-846-1	Sequence 1, Appl
10	1085	95.4	218	4 US-09-680-145-1	Sequence 1, Appl
11	1082	95.2	218	2 US-08-887-352B-15	Sequence 15, Appl
12	1082	95.2	218	2 US-08-887-352B-17	Sequence 17, Appl
13	1082	95.2	218	2 US-08-887-352B-19	Sequence 19, Appl
14	1082	95.2	218	2 US-08-887-352B-24	Sequence 24, Appl
15	1082	95.2	218	3 US-09-109-207C-15	Sequence 15, Appl
16	1082	95.2	218	3 US-09-109-207C-17	Sequence 17, Appl
17	1082	95.2	218	3 US-09-109-207C-19	Sequence 19, Appl
18	1082	95.2	218	3 US-09-109-207C-24	Sequence 24, Appl
19	1082	95.2	218	3 US-09-236-005-15	Sequence 15, Appl
20	1082	95.2	218	3 US-09-236-005-17	Sequence 17, Appl
21	1082	95.2	218	3 US-09-236-005-19	Sequence 19, Appl
22	1082	95.2	218	3 US-09-236-005-24	Sequence 24, Appl
23	1026	90.2	214	2 US-07-934-373C-39	Sequence 39, Appl
24	1026	90.2	214	3 US-08-437-642B-39	Sequence 39, Appl
25	1026	90.2	214	5 PCT-US93-07832-39	Sequence 39, Appl
26	1021	89.8	214	2 US-07-934-373C-40	Sequence 40, Appl
27	1021	89.8	214	2 US-08-788-800-11	Sequence 11, Appl

28	1021	89.8	214	3 US-08-437-642B-40	Sequence 40, Appl
29	1021	89.8	214	3 US-09-097-309-2	Sequence 2, Appl
30	1021	89.8	214	3 US-09-097-171A-2	Sequence 2, Appl
31	1021	89.8	214	4 US-09-460-587-2	Sequence 2, Appl
32	1021	89.8	214	5 PCT-US93-07832-40	Sequence 40, Appl
33	1021	89.8	233	2 US-07-934-373C-25	Sequence 25, Appl
34	1021	89.8	233	3 US-08-437-642B-25	Sequence 25, Appl
35	1021	89.8	233	4 US-08-146-206C-25	Sequence 25, Appl
36	1021	89.8	233	5 PCT-US93-07832-25	Sequence 25, Appl
37	1021	89.8	237	3 US-09-097-309-6	Sequence 6, Appl
38	1021	89.8	237	3 US-09-097-171A-10	Sequence 10, Appl
39	1021	89.8	237	3 US-09-422-112B-2	Sequence 2, Appl
40	1021	89.8	237	3 US-09-607-156-2	Sequence 2, Appl
41	1021	89.8	237	4 US-09-460-587-6	Sequence 6, Appl
42	1020	89.7	234	4 US-09-740-002-24	Sequence 24, Appl
43	1019.5	89.7	242	3 US-09-027-449-62	Sequence 62, Appl
44	1019.5	89.7	242	3 US-09-026-985-62	Sequence 62, Appl
45	1019.5	89.7	242	4 US-09-121-952A-62	Sequence 62, Appl

ALIGNMENTS

RESULT 1
PCT-US96-13152-2
; Application PC/TUS9613152
; GENERAL INFORMATION:
; APPLICANT: Martin, Ulrich, et al.
; TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ fai
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Felte & Lynch
; ADDRESSEE: Attn: Norman D. Hanson
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Computer Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/13152
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/578,953
; FILING DATE: 27-Dec-95
; APPLICATION NUMBER: EP 95 112 895.8
; FILING DATE: 17-Aug-95
; APPLICATION NUMBER: EP 95 114 969.9
; FILING DATE: 19-Sep-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Norman D. Hanson
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: BOER 1059-PCT-PFF/NDH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US96-13152-2
Query Match 100.0%; Score 1137; DB 5; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.5e-87; Indels 0; Gaps 0;
Matches 218; Conservative 0; Mismatches 0;

QY 1 DIQMTQSPSSLSASVGVDRVTITTCASQSVVDYDGSYNNMWYQKPKAKPKLLIYAASNL60
DB 1 DIQMTQSPSSLSASVGVDRVTITTCASQSVVDYDGSYNNMWYQKPKAKPKLLIYAASNL60
QY 61 GIPRFGSGSGGTDFTLTITSLQPEDPATYTCQSQNEDPMTFGGCTKVEIKRTVAAPSVF 120
DB 61 GIPRFGSGSGGTDFTLTITSLQPEDPATYTCQSQNEDPMTFGGCTKVEIKRTVAAPSVF 120
QY 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQSVTEQDSKOSTYSLS 180
DB 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQSVTEQDSKOSTYSLS 180
QY 181 STLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 218
DB 181 STLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 218

RESULT 2
US-08-887-352B-13
Sequence 13, Application US/08887352B
Patent No. 5994511
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-IgG Antibodies and Method of
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,352B
FILING DATE: 03-Jul-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-887-352B-13

Query Match 97.4%; Score 1108; DB 2; Length 218;
Best Local Similarity 97.2%; Pred. No. 4e-85; 1; Indels 0; Gaps 0;
Matches 212; Conservative 5; Mismatches 1;

QY 1 DIQMTQSPSSLSASVGVDRVTITTCASQSVVDYDGSYNNMWYQKPKAKPKLLIYAASNL60
DB 1 DIQMTQSPSSLSASVGVDRVTITTCASQSVVDYDGSYNNMWYQKPKAKPKLLIYAASNL60
QY 61 GIPRFGSGSGGTDFTLTITSLQPEDPATYTCQSQNEDPMTFGGCTKVEIKRTVAAPSVF 120
DB 61 GIPRFGSGSGGTDFTLTITSLQPEDPATYTCQSQNEDPMTFGGCTKVEIKRTVAAPSVF 120
QY 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQSVTEQDSKOSTYSLS 180
DB 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQSVTEQDSKOSTYSLS 180

QY 181 STLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 218
DB 181 STLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 218

RESULT 3
US-08-466-151-9
Sequence 9, Application US/08466151
Patent No. 6037453
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,151
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/466163
FILING DATE: 06-Jun-1995
APPLICATION NUMBER: 08/405617
FILING DATE: 15-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/185899
FILING DATE: 26-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/879495
FILING DATE: 07-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/744768
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P0718P2C1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-466-151-9

Query Match 97.4%; Score 1108; DB 3; Length 218;
Best Local Similarity 97.2%; Pred. No. 4e-85; 1; Indels 0; Gaps 0;
Matches 212; Conservative 5; Mismatches 1;

QY 1 DIQMTQSPSSLSASVGVDRVTITTCASQSVVDYDGSYNNMWYQKPKAKPKLLIYAASNL60
DB 1 DIQMTQSPSSLSASVGVDRVTITTCASQSVVDYDGSYNNMWYQKPKAKPKLLIYAASNL60
QY 61 GIPRFGSGSGGTDFTLTITSLQPEDPATYTCQSQNEDPMTFGGCTKVEIKRTVAAPSVF 120
DB 61 GIPRFGSGSGGTDFTLTITSLQPEDPATYTCQSQNEDPMTFGGCTKVEIKRTVAAPSVF 120
QY 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQSVTEQDSKOSTYSLS 180
DB 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQSVTEQDSKOSTYSLS 180

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 31, 2003, 10:29:11 ; Search time 17 Seconds

(without alignments)
2506.043 Million cell updates/sec

Title: US-09-917-410-4

Perfect score: 2357

Sequence: 1 EVQLVDSGGGVGPGGSLRL.....MREALNNHTYQKSLISLQK 443

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 76:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1743	73.9	327	1 G4HU	Ig gamma-4 chain C
2	1605.5	68.1	326	1 G2HU	Ig gamma-2 chain C
3	1590.5	67.5	330	1 GHU	Ig gamma-1 chain C
4	1585	67.2	377	2 A60764	Ig gamma-3 chain C
5	1575	66.8	377	2 A23511	Ig gamma-3 chain C
6	1519	64.4	470	2 S22080	Ig heavy chain pre
7	1495.5	63.4	444	2 PC4436	monoclonal antibod
8	1454	61.7	472	2 S31459	Ig gamma-1 chain -
9	1422.5	60.4	469	2 S37483	Ig gamma-2a chain
10	1417	60.1	446	2 S40295	Ig gamma-2a chain
11	1384	58.7	474	1 G2MS11	Ig gamma-2b chain
12	1348	57.2	374	2 S69339	Ig heavy chain V r
13	1331.5	56.5	475	2 S01321	Ig gamma-2b chain
14	1289.5	54.5	328	2 I47159	Ig gamma-2a chain
15	1283.5	54.5	328	2 I47160	Ig gamma-2b chain
16	1264.5	53.6	328	2 I47161	Ig gamma-2b chain
17	1240.5	52.6	328	2 I47158	Ig gamma-3 chain C
18	1199	50.9	323	1 GHRB	Ig gamma-1 chain C
19	1162	49.3	329	1 G2GP	Ig gamma-2 chain C
20	1147	48.7	308	2 C30554	Ig heavy chain C r
21	1139.5	48.3	255	4 S31866	Ig gamma-1 chain C
22	1129.5	47.9	234	2 P70207	Ig gamma chain C r
23	1124	47.7	333	2 PS0018	Ig gamma-2a chain
24	1118.5	47.5	326	2 PS0017	Ig gamma-1 chain C
25	1108.5	47.0	289	1 G3HUM1	Ig gamma-3 heavy C
26	1108	47.0	329	2 S00847	Ig gamma-2c chain
27	1106.5	46.9	324	1 G1MS	Ig gamma-1 chain C
28	1106.5	46.9	330	1 G2MSA	Ig gamma-2a chain
29	1104	46.8	548	2 S38864	Ig epsilon chain C

30	1103	46.8	327	2 S06611	Ig gamma-2 chain C
31	1101.5	46.7	393	1 G1MS	Ig gamma-1 chain C
32	1101.5	46.7	399	1 G2MSAM	Ig gamma-2a chain
33	1099	46.6	335	1 G2MSAB	Ig gamma-2a chain
34	1098.5	46.6	329	1 G3MSC	Ig gamma-3 chain C
35	1090.5	46.3	398	1 G3MSM	Ig gamma-3 chain C
36	1085.5	46.1	277	2 I47162	Ig gamma-4 chain C
37	1084.5	46.0	322	2 PS0019	Ig gamma-2a chain
38	1049.5	44.5	505	1 G2MSBM	Ig gamma-2b chain
39	899.5	38.2	249	2 S04845	Ig heavy chain pre
40	872.5	37.0	249	2 S69340	Ig heavy chain VHI
41	861.5	36.6	572	2 B46529	Ig Y heavy chain (
42	825.5	35.0	241	2 S69131	Ig heavy chain (DO
43	805	34.2	218	2 A36040	Ig heavy chain V-I
44	768.5	32.6	220	2 A49444	Ig gamma-1 heavy C
45	767	32.5	627	2 S14683	Ig mu chain precur

ALIGNMENTS

RESULT 1

G4HU

Ig gamma-4 chain C region - human

C/Species: Homo sapiens (man)

C/Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #ext_change 16-Jul-1999

C/Accession: A90933; A90249; A02150

R/Ellison, J.; Buxbaum, J.; Hood, L.

DNA 1, 11-18, 1981

A/Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.

A/Reference number: A90933; PMID:83157104; PMID:6299662

A/Accession: A90933

A/Molecule type: DNA

A/Residues: 1-327 <EL>

A/Note: the sequence was determined from the germline gene

R/Pink, J.R.L., Buttery, S.H.; De Vries, G.M.; Milstein, C.

Biochem. J. 117, 33-47, 1970

A/Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant

A/Reference number: A90249; PMID:70207560; PMID:4192699

A/Molecule type: protein

A/Residues: 130,81-326 <PIN>

C/Genetics:

A/Gene: GDB:IGHG4

A/Cross-references: GDB:119340; OMIM:147130

A/Map position: 14q32.33-14q32.33

Query Match 73.9%; Score 1743; DB 1; Length 327;

Best Local Similarity 100.0%; Pred. No. 1.2e-93;

Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 117 ASKRGSPVPLAPCSSTSESTRALGCVKDYRPEVTSWNSGALTSGVHTFPALQSS 176

DB 1 ASKRGSPVPLAPCSSTSESTRALGCVKDYRPEVTSWNSGALTSGVHTFPALQSS 60

QY 177 GUYSLSSVTVTPSSSLGTITTCNVDHKPSNFKVDKRVESKYGPPCPSPAPAFGLGSPV 236

DB 61 GUYSLSSVTVTPSSSLGTITTCNVDHKPSNFKVDKRVESKYGPPCPSPAPAFGLGSPV 120

QY 237 PLFPPKPKDTLMISRTPEVTCVVVDVSDPEDEVQFNWYVDGVEVHNAKTKPREEQFNSTY 296

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Db      121  FLFPKPKDLMISRTPEVTCVVVDVSDPEDEVDFNMVVDVEVHNATKTRPEEQFNSTY 180
      297  RVSVLVTLVHODMNGEKYCKVKVSKGLPSSIEKTIISAKGQPREPOVYTLPPSQQEMTK 356
      181  RVSVLVTLVHODMNGEKYCKVKVSKGLPSSIEKTIISAKGQPREPOVYTLPPSQQEMTK 240
      357  NVSVLTLVKGFPYPSDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSRLTVDKSRWQEG 416
      241  NVSVLTLVKGFPYPSDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSRLTVDKSRWQEG 300
      417  NVFSCSVMEALHNHYTQKSLSLSTGK 443
      301  NVFSCSVMEALHNHYTQKSLSLSTGK 327

RESULT 2
G2HU
IG Gamma-2 chain C region - human
C/Species: Homo sapiens (man)
C/Date: 30-Apr-1981 #sequence revision 13-Jun-1983 #text_change 21-Jul-2000
C/Accession: A93906; A92809; A90752; A93132; A02148
R:Ellison, J.; Hood, L. U.S.A. 79, 1984-1988, 1982
A/Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain c
A/Reference number: A93906; MUID:82197621; PMID:6804948
A/Accession: A93906
A/Molecule type: DNA
A/Residues: 1-326 <ELL>
A/Cross-references: GB:V00554; GB:J00230; NID:932759; PIDN:CB58438.1; PID:ig6066056
A/Note: Lys-326 is probably removed posttranslationally
R:Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A/Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f
A/Reference number: A92809; MUID:81007873; PMID:6774012
A/Accession: A92809
A/Contents: myeloma protein T11
A/Molecule type: protein
A/Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <WAN>
A/Note: Trp-156 is at or near the complement-binding site
R:Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A/Title: The amino acid sequences of the three heavy chain constant region domains of a
A/Reference number: A90752; MUID:80001357; PMID:113060
A/Accession: A90752
A/Contents: myeloma protein Z1e
A/Molecule type: protein
A/Residues: 1-24, 'E', 26-57, 'EV', 60-85, 132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 198-
A/Note: this sequence has been revised
R:Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A/Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g
A/Reference number: A93132; MUID:80114419; PMID:118920
A/Accession: A93132
A/Contents: Z1e
A/Molecule type: protein
A/Residues: 238-275 <HOF>
R:Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A/Reference number: A94591
A/Contents: annotation; Z1e, revisions to residues 25, 59, 60, and 264-268
A/Note: the revised sequence differs from that shown in having 60-Ala and in the amidat
ned
R:Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A/Title: Disulfide bridges of the heavy chain of human immunoglobulin G2.
A/Reference number: A90253; MUID:72033500; PMID:4940472
A/Contents: annotation; myeloma protein Sa, disulfide bonds
R:Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A/Title: Structural studies of immunoglobulin G.
A/Reference number: A93157; MUID:69064124; PMID:5782707
A/Contents: annotation; Sa, disulfide bonds

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C/Genetics:
A/Gene: GDB:119338; OMIM:147110
A/Cross-references: GDB:119338; OMIM:147110
A/Map position: 14q32.33-14q32.33
A/Complex: An immunoglobulin heterotrimer subunit consists of two identical light (ka
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1
C/Superfamily: Immunoglobulin C region; immunoglobulin homology
C/Keywords: duplication; glycoprotein; heterotrimer; immunoglobulin
F/20-85/Domain: immunoglobulin homology <IM1>
F/133-202/Domain: immunoglobulin homology <IM2>
F/239-306/Domain: immunoglobulin homology <IM3>
F/14/Disulfide bonds: interchain (to light chain) #status experimental
F/27-83,140-200,246-304/Disulfide bonds: #status experimental
F/102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F/176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match      68.1%; Score 1605.5; DB 1; Length 326;
Best Local Similarity 92.4%; Pred. No. 1e-85;
Matches 302; Conservative 10; Mismatches 14; Indels 1; Gaps 1;

Db      117  ASTKGPVFPFLAPCSRSTSESTALGCLVDYDPEPYVSMNSGALTSGVHTPPAVLQSS 176
      1  ASTKGPVFPFLAPCSRSTSESTALGCLVDYDPEPYVSMNSGALTSGVHTPPAVLQSS 60
      177  GLYSLSVTVTPSSSGCTKTYTCNVDRKPSNTKYDKRVESKYGPCCPCAPFLGSPSV 236
      61  GLYSLSVTVTPSSNFGTYTCNVDRKPSNTKYDKRVESKYGPCCPCAPFLGSPSV 119
      237  FLFPKPKDLMISRTPEVTCVVVDVSDPEDEVDFNMVVDVEVHNATKTRPEEQFNSTY 296
      120  FLFPKPKDLMISRTPEVTCVVVDVSDPEDEVDFNMVVDVEVHNATKTRPEEQFNSTY 179
      297  RVSVLVTLVHODMNGEKYCKVKVSKGLPSSIEKTIISAKGQPREPOVYTLPPSQQEMTK 356
      180  RVSVLVTLVHODMNGEKYCKVKVSKGLPAPIEKTIISKQPREPOVYTLPPSQQEMTK 239
      357  NVSVLTLVKGFPYPSDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSRLTVDKSRWQEG 416
      241  NVSVLTLVKGFPYPSDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSRLTVDKSRWQEG 299
      417  NVFSCSVMEALHNHYTQKSLSLSTGK 443
      300  NVFSCSVMEALHNHYTQKSLSLSTGK 326

RESULT 3
G2HU
IG Gamma-1 chain C region - human
C/Species: Homo sapiens (man)
C/Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text_change 16-Jul-1999
C/Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146
R:Ellison, J.W.; Beron, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
A/Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.
A/Reference number: A93433; MUID:82274238; PMID:6287432
A/Accession: A93433
A/Molecule type: DNA
A/Residues: 1-330 <ELL>
A/Cross-references: EMBL:Z17370
A/Note: this sequence has the Gln(17) alleotypic marker, 97-Lys, and the Gln(1) markers,
A/Note: Lys-330 is removed after translation
R:Harris, L.J.
submitted to the EMBL Data Library, October 1992
A/Reference number: S33904
A/Accession: S36861
A/Molecule type: DNA
A/Residues: 2-330 <HAR>
A/Cross-references: EMBL:Z17370
R:Takahashi, N.; Ueda, S.; Obata, M.; Nikaide, T.; Nakai, S.; Honjo, T.
Cell 29, 671-679, 1982
A/Title: Structure of human immunoglobulin gamma genes: implications for evolution of e
A/Reference number: S33887; MUID:83001943; PMID:6811139
A/Accession: S33887

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FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 27 83
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 141 201
 FT DISULFID 247 305
 SQ SEQUENCE 327 AA; 35940 MW; 3EDBD11EF208E7A CRC64;
 Query Match 73.9%; Score 1743; DB 1; Length 327;
 Best Local Similarity 100.0%; Pred. No. 2e-114;
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 117 ASTGSPVFPPLAPCRSTSESTALGCLVXYFPEPVTVNNSGMLTSGVTFPPVLDSS 176
 DB 1 ASTGSPVFPPLAPCRSTSESTALGCLVXYFPEPVTVNNSGMLTSGVTFPPVLDSS 60
 QY 177 GLYSLSVVTVPSSSLGRTKTYTCNVDRHKPSMTKVDRVSKYKGPSPCPAPPEFLGGPSV 236
 DB 61 GLYSLSVVTVPSSSLGRTKTYTCNVDRHKPSMTKVDRVSKYKGPSPCPAPPEFLGGPSV 120
 QY 237 FLFPEPKPDTLMISRTPEVTCVVDVDSQEDPEVQFNMYVDGVEVNAKTKPREQFNSTY 296
 DB 121 FLFPEPKPDTLMISRTPEVTCVVDVDSQEDPEVQFNMYVDGVEVNAKTKPREQFNSTY 180
 QY 297 RVSVTLTVLHODMLNGKIKCKVSNKGLPSSIEKTIISAKGQPREPQYTLPPSQEEMTK 356
 DB 181 RVSVTLTVLHODMLNGKIKCKVSNKGLPSSIEKTIISAKGQPREPQYTLPPSQEEMTK 240
 QY 357 NOVSLTCLVKGFPSPDIWVEMSNQPPNNYKTPPVLDSSGFLYRLTVDSKRMQEG 416
 DB 241 NOVSLTCLVKGFPSPDIWVEMSNQPPNNYKTPPVLDSSGFLYRLTVDSKRMQEG 300
 QY 417 NVFSCSVMEHALNHNHYTKSLSLSLGK 443
 DB 301 NVFSCSVMEHALNHNHYTKSLSLSLGK 327
 RESULT 2
 GC2_HUMAN STANDARD; PRT; 326 AA.
 AC P01859;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ig gamma-2 chain C region.
 GN IGHG2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 OX [1]
 RP SEQUENCE OF 2-326 FROM N.A.
 RX MEDLINE=82197621; PubMed=6804948;
 RA Ellison J.W., Hood L.E.;
 RT "Linkage and sequence homology of two human immunoglobulin gamma
 RT heavy chain constant region genes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).
 RN [2]
 RP SEQUENCE OF 88-115 FROM N.A.
 RX TISSUE=Fetal liver;
 RX MEDLINE=83001943; PubMed=6811139;
 RA Takahashi N., Ueda S., Obata M., Nikaido T., Nakai S., Honjo T.;
 RT "Structure of human immunoglobulin gamma genes: implications for
 RT evolution of a gene family.";
 RL Cell 29:671-679(1982).
 RN [3]
 RP SEQUENCE OF 99-177 AND 310-326 FROM N.A.
 RX TISSUE=Fetal liver;
 RX MEDLINE=84235992; PubMed=6329676;
 RA Krawinkel U., Rablites T.H.;
 RT "Comparison of the hinge-coding segments in human immunoglobulin gamma
 RT heavy chain genes and the linkage of the gamma 2 and gamma 4 subclasses
 RT genes."

RL EMBL J. 1:403-407(1982).
 RN [4]
 RP SEQUENCE OF 1-325 (MYELOMA PROTEIN T1L).
 RX MEDLINE=81007873; PubMed=6774012;
 RA Wang A.-C., Tung B., Fudenberg H.H.;
 RT "The primary structure of a human IgG2 heavy chain: genetic,
 RT evolutionary, and functional implications.";
 RL J. Immunol. 125:1048-1054(1980).
 RN [5]
 RP SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN Z1E).
 RX MEDLINE=80001357; PubMed=113060;
 RA Connell G.E., Parr D.M., Hofmann T.;
 RT "The amino acid sequences of the three heavy chain constant region
 RT domains of a human IgG2 myeloma protein.";
 RL Can. J. Biochem. 57:758-767(1979).
 RN [6]
 RP SEQUENCE OF 238-275 (Z1E).
 RX MEDLINE=80114419; PubMed=118920;
 RA Hofmann T., Parr D.M.;
 RT "A note of the amino acid sequence of residues 381-391 of human
 RT immunoglobulin gamma chains.";
 RL Mol. Immunol. 16:923-925(1979).
 RN [7]
 RP REVISIONS TO 25; 59; 60 AND 264-268 (Z1E).
 RA Hofmann T., Parr D.M.;
 RL Submitted (MAR-1980) to the PIR data bank.
 RN [8]
 RP SEQUENCE OF 1-121 (DOT).
 RX MEDLINE=9525298; PubMed=7737190;
 RA Stoppani M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
 RT "Characterization of the two unique human anti-flavin monoclonal
 RT immunoglobulins.";
 RL Eur. J. Biochem. 228:886-893(1995).
 RN [9]
 RP DISULFIDE BONDS.
 RX MEDLINE=72033500; PubMed=4940472;
 RA Milstein C., Frangione B.;
 RT "Disulphide bridges of the heavy chain of human immunoglobulin G2.";
 RL Biochem. J. 121:217-225(1971).
 RN [10]
 RP DISULFIDE BONDS.
 RX MEDLINE=69064124; PubMed=5782707;
 RA Frangione B., Milstein C., Pink U.R.L.;
 RT "Structural studies of immunoglobulin G.";
 RL Nature 221:145-148(1969).
 CC -----
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 CC -----
 DR EMBL; J00230; AAB59393.1; -;
 DR PIR; A93906; G2HU.
 DR HSSP; P01857; 1PC1.
 DR Genew; HGNC:5526; IGHG2.
 DR MIM; 147110; -;
 DR GO; GO:0005624; C:membrane fraction; NAS.
 DR GO; GO:0003823; F:antigen binding activity; TNS.
 DR GO; GO:0006955; F:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00407; Igcl; 2.
 DR PROSITE; PS00835; IG_LIKE; 3.
 DR PROSITE; PS00290; IG_MHC; 2.
 KW Immunoglobulin domain; Immunoglobulin C region.
 FT NON TER 1 98 CH1.
 FT DOMAIN 99 110 HINGE.

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OM protein - protein search, using sw model

Run on: December 31, 2003, 10:29:10 ; Search time 37.6667 Seconds

(without alignments)
3034.973 Million cell updates/sec

Title: us-09-917-410-4

Perfect score: 2357 1 EVOLVESGGGLVPGGSLRL.....MHKALNNHTYQKSLSLGK 443

Sequence: 1 EVOLVESGGGLVPGGSLRL.....MHKALNNHTYQKSLSLGK 443

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP virus:*
16: SP bacteriophage:*
17: SP archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2091.5	88.7	471	4	08TC77
2	2032	86.2	473	4	08TC63
3	1990.5	84.5	521	4	08N4Y9
4	1571	66.7	509	4	08N1F7
5	1557.5	66.1	469	11	08R3V9
6	1547.5	65.7	437	11	09R1A4
7	1515.5	64.3	473	11	091Z05
8	1471.5	62.4	473	11	09D8L4
9	1458.5	61.9	463	11	0991C4
10	1432	60.8	468	11	0991J1
11	1405.5	59.6	473	11	0991L25
12	1376	58.4	474	11	08R3H6
13	1217	51.6	337	6	09SM34
14	1149.5	48.8	701	4	096P08
15	967.5	41.0	597	4	096BB9
16	929	39.4	613	4	08WUK1

17	876.5	37.2	487	11	099KA4	099KA4 mus musculu
18	868	36.8	494	4	096K68	096K68 homo sapien
19	852.5	36.2	499	4	08N5K4	08N5K4 homo sapien
20	846.5	35.9	493	4	08NCL6	08NCL6 homo sapien
21	836	35.5	486	11	091Z07	091Z07 mus musculu
22	820.5	34.8	479	11	091WPS	091WPS mus musculu
23	788.5	33.5	480	11	091XEL	091XEL mus musculu
24	772	32.8	484	11	08VEA0	08VEA0 mus musculu
25	764.5	32.4	614	4	096GA6	096GA6 homo sapien
26	758.5	32.2	597	4	09BUI0	09BUI0 homo sapien
27	754	32.0	613	4	096EY0	096EY0 homo sapien
28	752.5	31.9	597	4	09B0B8	09B0B8 homo sapien
29	748.5	31.8	588	4	08WUX4	08WUX4 homo sapien
30	746.5	31.8	618	4	096FA6	096FA6 homo sapien
31	746	31.7	613	11	08VCX7	08VCX7 mus musculu
32	735	31.2	278	11	0921X1	0921X1 mus musculu
33	724	30.7	482	11	091X92	091X92 mus musculu
34	707	30.0	500	4	09BRV0	09BRV0 homo sapien
35	704	29.9	496	4	096KX8	096KX8 homo sapien
36	701	29.7	573	4	08WU38	08WU38 homo sapien
37	697	29.6	484	11	099LA6	099LA6 mus musculu
38	689.5	29.3	497	4	08WY24	08WY24 homo sapien
39	685	29.1	482	11	08K172	08K172 mus musculu
40	685	29.1	486	4	096DK0	096DK0 mus sapien
41	678	28.8	480	11	08K0Z4	08K0Z4 mus musculu
42	675.5	28.7	481	11	091WT1	091WT1 mus musculu
43	674	28.6	488	11	091WR1	091WR1 mus musculu
44	665.5	28.2	489	11	08VCX4	08VCX4 mus musculu
45	665	28.2	488	11	08K0F2	08K0F2 mus musculu

ALIGNMENTS

RESULT 1

ID 08TC77 PRELIMINARY; PRT; 471 AA.
AC 08TC77;
DT 01-JUN-2002 (TEMBLrel. 21, Created)
DT 01-JUN-2002 (TEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Splice;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC024289; AAH24289.1; -
DR InterPro; IPR007110; IG_11ke.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_4.
DR SMART; SM00406; IG_V.1.
DR PROSITE; PSS0835; IG_LIKE; 4.
DR PROSITE; PSS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 471 AA; 51791 MW; 388F7F4CF588660E CRC64;

Query Match 88.7%; Score 2091.5; DB 4; Length 471;

Best local similarity 88.3%; Pred. No. 8.8e-166; Mismatches 399; Conservative 21; Mismatches 23; Indels 9; Gaps 3;

QY 1 EVOLVESGGGLVPGGSLRLISCAAGFTSTYAMSWVRQAQPGKLEWVASISTGGS-TYY 59
DB 20 EVOLVESGGGLVPGGSLRLISCAAGFTSTYAMSWVRQAQPGKLEWVASISTGGS-TYY 79
QY 60 PDSVKGRFTTSRMAKNTLYLQNSLRAPETAYYGCARDV-----GYPPWQCGTLVYV 114
DB 80 ADSVKGRFTTSRMAKNTLYLQNSLRAPETAYYGCARDVRLQTLTSYWFEDLWGRGTLVYV 139

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Qy 115 SSASTKGPVPEPLAPCSRSTSESTALGCLVKDYFPEPVTVSNMGSALTSGVHTFPAVLQ 174
Db 140 SSASTKGPVPEPLAPCSRSTSESTALGCLVKDYFPEPVTVSNMGSALTSGVHTFPAVLQ 199
Qy 175 SSGLYSLSSVTVTVSSSLGTYTCYCNVDHKPSNTKVDKRVSK--YGPCCPAPBFL 231
Db 200 SSGLYSLSSVTVTVSSSLGTYTCYCNVDHKPSNTKVDKRVSKCDKTHTCPPCAPBFL 259
Qy 232 GGPVPEPLAPKPTLMISRTPEVTCVVDVSOEPEVQFMVYDGVENHAKTKPREQ 291
Db 260 GGPVPEPLAPKPTLMISRTPEVTCVVDVSHEDPEVQFMVYDGVENHAKTKPREQ 319
Qy 292 FNSTYRVSVTLVTHQDWLNGEKYCKVSNKGLPSSIEKTISSAKGQPREPQVYTLPPSQ 351
Db 320 YNSTYRVSVTLVTHQDWLNGEKYCKVSNKGLPSSIEKTISSAKGQPREPQVYTLPPSR 379
Qy 352 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSLRTVDS 411
Db 380 DELTGNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSLRTVDS 439
Qy 412 RMQGNVFCGVMEALHNHYTOKSLSLGK 443
Db 440 RMQGNVFCGVMEALHNHYTOKSLSLGK 471

RESULT 2
Q8TC63 PRELIMINARY; PRT: 473 AA.
ID Q8TC63,
AC Q8TC63,
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue-Kidney;
RA Strauberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025985; AAH25985.1; -
DR InterPro; IPR000923; BlueGL.1.
DR InterPro; IPR007110; Ig-Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00196; COPPER_BLUE; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 3.
KM Hypothetical protein.
SQ SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;

Query Match 86.2%; Score 2032; DB 4; Length 473;
Best Local Similarity 86.1%; Pred. No. 86-161;
Matches 384; Conservative 24; Mismatches 34; Indels 4; Gaps 2;

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Db 208 LYSLSVTVTVSSSLGTYTCYCNVDHKPSNTKVDKRVSKYGPCCPAPBFLGSPVF 267
Qy 238 LFPKPKDTLMISRTPEVTCVVDVSOEPEVQFMVYDGVENHAKTKPREQFNSTYR 297
Db 268 LFPKPKDTLMISRTPEVTCVVDVSOEPEVQFMVYDGVENHAKTKPREQFNSTYR 327
Qy 298 VSVTLVTHQDWLNGEKYCKVSNKGLPSSIEKTISSAKGQPREPQVYTLPPSQEEMTKN 357
Db 328 VSVTLVTHQDWLNGEKYCKVSNKGLPSSIEKTISSAKGQPREPQVYTLPPSQEEMTKN 387
Qy 358 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSLRTVDSRMQGN 417
Db 388 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSLRTVDSRMQGN 447
Qy 418 VFSCGVMEALHNHYTOKSLSLGK 443
Db 448 VFSCGVMEALHNHYTOKSLSLGK 473

RESULT 3
Q8N4Y9 PRELIMINARY; PRT: 521 AA.
ID Q8N4Y9,
AC Q8N4Y9,
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue-Primary B-Cells from Tonsils;
RA Strauberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC033178; AAH33178.1; -
DR InterPro; IPR007110; Ig-Like.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_4.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KM Hypothetical protein.
SQ SEQUENCE 521 AA; 57156 MW; 2AC7D22E72DCAA2 CRC64;

Query Match 84.5%; Score 1990.5; DB 4; Length 521;
Best Local Similarity 76.5%; Pred. No. 2.6e-157;
Matches 384; Conservative 24; Mismatches 35; Indels 59; Gaps 3;

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OM protein - protein search, using sw model

Run on: December 31, 2003, 10:33:16 ; Search time 45.6667 Seconds

(Without alignments)
1539.764 Million cell updates/sec

Title: US-09-917-410-4

Perfect score: 2357
Sequence: 1 EVOLVESGGGLVPGGSLRL.....MHEALHNHYTQKSLSLGLK 443

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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24: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2357	100.0	443	AAW13564	Humanised anti-L-6
2	2253.5	95.6	467	AA80617	Anti-human IL-4 hu
3	2139	90.8	447	AAW10232	TF8-569 CDR-grafte
4	2123.5	90.1	467	ABP71365	Anti-OpGL-1 antiIdo
5	2120.5	90.0	447	AAE33522	Human AQC2 heavy c
6	2120	89.9	470	ABG77158	German protein s
7	2114.5	89.7	447	AAE33523	Human AQC2 heavy c
8	2113.5	89.7	447	AAE33524	Human AQC2 heavy c
9	2113	89.6	474	AAO14065	Heavy chain protei

10	2113	89.6	474	24	ABU08017	Human monoclonal r
11	2111	89.6	449	21	AAI68810	A rat heavy chain
12	2109.5	89.5	449	23	AAO18400	Mature humanised m
13	2105	89.3	449	24	ABP58273	Humanised 3D6 anti
14	2105	89.3	468	24	ABP58275	Humanised 3D6 anti
15	2101	89.1	470	23	ABG77157	Human acid sequenc
16	2098.5	89.0	444	24	ABG77157	BIM4/8 antibody h
17	2096.5	88.9	442	24	ABE80109	Heavy chain. Homo
18	2096.5	88.9	442	24	ABR39465	Humanised anti-Abe
19	2096.5	88.9	442	24	ABU08311	Humanised 266 anti
20	2096.5	88.9	461	22	AAU07745	Humanised monoclon
21	2096	88.9	468	13	AAE28808	pre-5A8 humanised
22	2093	88.8	470	23	AAU74298	Anti-human AILIM m
23	2093	88.8	470	23	AAU74300	Anti-human AILIM m
24	2090	88.7	451	22	AAE12715	Human recombinant
25	2090	88.7	451	24	ABU58807	Mucin 1 (MUC-1) bi
26	2089.5	88.7	473	23	ABG77162	Germine protein s
27	2089.5	88.7	477	22	AAU14288	Human novel protei
28	2087.5	88.6	463	21	AAU93707	The heavy chain of
29	2087.5	88.6	463	21	AAU93732	The heavy chain of
30	2086.5	88.5	442	24	ABR80113	Deglycosylated hea
31	2086.5	88.5	442	24	ABR39474	Humanised anti-Abe
32	2086.5	88.5	442	24	ABU08320	Humanised antibody
33	2083	88.4	464	21	AAU93703	The heavy chain of
34	2083	88.4	464	21	AAU93730	The heavy chain of
35	2083	88.4	464	21	AAU93730	The heavy chain of
36	2081.5	88.3	463	21	ABG77161	Amino acid sequenc
37	2081.5	88.3	463	21	AAU93701	The heavy chain of
38	2081	88.3	451	21	AAU93727	The heavy chain of
39	2080.5	88.3	451	21	AAU93734	The heavy chain of
40	2078	88.2	464	24	ABP96294	4A5-3.1.1-B4 anti b
41	2078	88.2	464	18	AAW14941	3F4 Human IgG4 exp
42	2078	88.2	464	18	AAW14938	Murine anti-porcine
43	2076	88.1	562	22	AAE81987	Ganglioside GD3 sp
44	2075.5	88.1	466	13	AAE24812	Sequence encoded b
45	2071	87.9	463	21	AAU93728	The heavy chain of
			462	22	AAE72234	Humanised 323/A3 (

ALIGNMENTS

RESULT 1	
AAW13564	standard; Protein; 443 AA.
ID	AAW13564
XX	
AC	AAW13564;
XX	
DT	03-JUN-1997 (first entry)
XX	
DE	Humanised anti-L-selectin antibody Hudreg 55 heavy chain.
XX	
KW	L-selectin; humanised antibody; Hudreg 55; acute organ damage;
KW	organ failure; poly-trauma; haemorrhagic-traumatic shock.
XX	
OS	Chimeric Mus sp.;
OS	Chimeric Homo sapiens.
XX	
PN	WO9706822-A1.
XX	
PD	27-FEB-1997.
XX	
PF	14-AUG-1996; 96WO-US13152.
XX	
PR	27-DEC-1995; 95US-0578953.
PR	17-AUG-1995; 95EP-0112895.
PR	19-SEP-1995; 95EP-0114696.
XX	
PA	(BOEF) BOEHRINGER MANNHEIM GMBH.
PA	(PROT-) PROTEIN DESIGN LABS INC.
XX	
PI	Co M, Haselbeck A, Martin U, Schumacher G;
DR	WPI; 1997-165036/15.

DR N-PSDB; AAT61281.
 XX Using anti-selectin antibody to prevent acute organ damage and
 PT multiple organ failure - during extracorporeal circulation or
 PT following polytrauma, e. g. haemorrhagic-traumatic shock
 XX
 PS Disclosure; Page 34-36; 52pp; English.
 XX
 CC Humanised anti-L-selectin antibody Hddreg 55 comprises 2 heavy
 CC chains each having the sequence given in AAW13564 and 2 light chains
 CC each having the sequence given in AAW13563. These are encoded by the
 CC cDNA clones given in AAT61281 and AAT61280. Hddreg 55 can be used to
 CC prevent multiple organ failure associated with polytrauma and for
 CC the prevention of acute organ damage associated with extracorporeal
 CC blood circulation. The antibody inhibits interaction between the
 CC carbohydrate-recognising domain of the selectin and the
 CC corresponding cell surface receptor.
 XX
 SQ Sequence 443 AA;
 Query Match 100.0%; Score 2357; DB 18; Length 443;
 Best Local Similarity 100.0%; Pred. No. 5,4e-137;
 Matches 443; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMSWVRQAPGKGLEWVASISTGSTYYP 60
 DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMSWVRQAPGKGLEWVASISTGSTYYP 60
 QY 61 DSVKRRFTISRDNAAKNTLYLQNNSLRAEDTAVYYCARIDYDGFYWGQGLTVTVSSASTK 120
 DB 61 DSVKRRFTISRDNAAKNTLYLQNNSLRAEDTAVYYCARIDYDGFYWGQGLTVTVSSASTK 120
 QY 121 GPSVPEPLAPCSRSTSESTALGCLVKDYFPEPVTVSNMGSALTSGVHTFPAVLQSSGLYS 180
 DB 121 GPSVPEPLAPCSRSTSESTALGCLVKDYFPEPVTVSNMGSALTSGVHTFPAVLQSSGLYS 180
 QY 181 LSSVTVTPSSSLGTYTTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGSPVFLFP 240
 DB 181 LSSVTVTPSSSLGTYTTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGSPVFLFP 240
 QY 241 PRPKDTLMISRTPEVTCVVDVSOEDPEVQFMWYVDGVEVNAKTRPREEOFNSTYRVVS 300
 DB 241 PRPKDTLMISRTPEVTCVVDVSOEDPEVQFMWYVDGVEVNAKTRPREEOFNSTYRVVS 300
 QY 301 VLTVLHODMLNGKEYKCKVSNKGLPSSIEKTISSAKGQPREPOVYTLPPSQEEMTKNQVS 360
 DB 301 VLTVLHODMLNGKEYKCKVSNKGLPSSIEKTISSAKGQPREPOVYTLPPSQEEMTKNQVS 360
 QY 361 LTCLVKGFPYPSDIAVWESNGQPENNYKTTTPVLDSGSEFLYSRLTVDKSRMDEGNVFS 420
 DB 361 LTCLVKGFPYPSDIAVWESNGQPENNYKTTTPVLDSGSEFLYSRLTVDKSRMDEGNVFS 420
 QY 421 CSVMHEALHNHYTQKSLSLSTLCK 443
 DB 421 CSVMHEALHNHYTQKSLSLSTLCK 443

RESULT 2
 AAR80617
 ID AAR80617 standard; Protein; 467 AA.
 XX
 AC AAR80617;
 XX
 DT 19-APR-1996 (first entry)
 XX
 DE Anti-human IL-4 humanised MAb h25D2-9 mature heavy chain.
 XX
 KW Anti-human interleukin-4; IL-4; humanised; purification;
 XX treatment; IL-4 diseases; immunoassay; heavy chain; h25D2-9;
 XX antibody.
 XX
 OS Homo sapiens.
 XX

EH Key Location/Qualifiers
 FT Peptide 1..19
 FT /label= leader_sequence
 FT Peptide 20..467
 FT /label= mat_peptide
 XX
 XX MO9524481-A2.
 XX
 XX 14-SEP-1995.
 XX
 XX 08-MAR-1995; 95WO-US02400.
 XX
 XX 10-MAR-1994; 94US-0208886.
 XX
 XX (SCHE) SCHERING CORP.
 XX
 PI Dalie B, Miller K, Murgolo N, Tindall S;
 XX
 DR WPI; 1995-328272/42.
 XX
 PT Humanised monoclonal antibody against human interleukin (IL)-4 -
 PT has increased binding affinity and expression, and hence greater
 PT therapeutic value in the treatment of IL-4 related diseases
 XX
 XX Claim 3; Pages 109-110; 116pp; English.
 PS
 CC AAR80617 is the anti-human IL-4 humanised monoclonal antibody (MAb)
 CC h25D2-9, mature heavy chain. It can be used for the prepn.,
 CC purificn. and immunoassay of the humanised Abs. Pharmaceutical
 CC compns. and anti-idiotypic Abs (against the MAb) can also be
 CC prepd. for the treatment of IL-4 related diseases by respectively
 CC suppressing, or imitating the binding activity of IL-4. The
 CC humanised MAb is derived from the rodent. MAb 25D2.
 CC
 SQ Sequence 467 AA;
 Query Match 95.6%; Score 2253.5; DB 16; Length 467;
 Best Local Similarity 95.3%; Pred. No. 1.3e-130;
 Matches 427; Conservative 11; Mismatches 5; Indels 5; Gaps 3;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMSWVRQAPGKGLEWVASIS-TGSGSTY 59
 DB 20 EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMSWVRQAPGKGLEWVASIS-TGSGSTY 79
 QY 60 PDSVKGKFTISRDNAAKNTLYLQNNSLRAEDTAVYYCARD--YDG-YFDYWGQGLTVVS 115
 DB 80 PDSVKGKFTISRDNAAKNTLYLQNNSLRAEDTAVYYCARDYFEGHYFDYWGQGLTVVS 139
 QY 116 SASIKGSPVPEPLAPCSRSTSESTALGCLVKDYFPEPVTVSNMGSALTSGVHTFPAVLQ 175
 DB 140 SASIKGSPVPEPLAPCSRSTSESTALGCLVKDYFPEPVTVSNMGSALTSGVHTFPAVLQ 199
 QY 176 SGLYSLSVTVTPSSSLGTYTTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGSPS 235
 DB 200 SGLYSLSVTVTPSSSLGTYTTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGSPS 259
 QY 236 VFLPFPKDTLMISRTPEVTCVVDVSOEDPEVQFMWYVDGVEVNAKTRPREEOFNST 295
 DB 260 VFLPFPKDTLMISRTPEVTCVVDVSOEDPEVQFMWYVDGVEVNAKTRPREEOFNST 319
 QY 296 YRVVSVLTVLHODMLNGKEYKCKVSNKGLPSSIEKTISSAKGQPREPOVYTLPPSQEEMT 355
 DB 320 YRVVSVLTVLHODMLNGKEYKCKVSNKGLPSSIEKTISSAKGQPREPOVYTLPPSQEEMT 379
 QY 356 KNQVSLTCLVKGFPYPSDIAVWESNGQPENNYKTTTPVLDSGSEFLYSRLTVDKSRMDE 415
 DB 380 KNQVSLTCLVKGFPYPSDIAVWESNGQPENNYKTTTPVLDSGSEFLYSRLTVDKSRMDE 439
 QY 416 GNVSFCSVMHEALHNHYTQKSLSLSTLCK 443
 DB 440 GNVSFCSVMHEALHNHYTQKSLSLSTLCK 467

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 31, 2003, 10:32:16 ; Search time 34.3333 Seconds

(without alignments)
2588.856 Million cell updates/sec

Title: US-09-917-410-4

Perfect score: 2357
Sequence: 1 EVQLVESGGGLVQPGGSLRL.....MHEALHNHYTQKSISLSLGR 443

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 733937 seqs, 200641211 residues

Total number of hits satisfying chosen parameters: 733937

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubppaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubppaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubppaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubppaa/US08_NEW_PUB.pep:*
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11: /cgn2_6/ptodata/1/pubppaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubppaa/US09_NEW_PUB.pep:*
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15: /cgn2_6/ptodata/1/pubppaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2357	100.0	443	9	US-09-917-410-4
2	2266.5	96.2	465	12	US-10-401-344-2
3	2113	89.6	474	12	US-10-225-108A-3
4	2112	89.6	474	12	US-09-848-832-3
5	2112.5	89.6	445	12	US-10-320-231A-79
6	2111	89.6	449	10	US-09-736-371B-21
7	2106.5	89.4	448	9	US-09-917-410-6
8	2098.5	89.0	444	15	US-10-150-475A-6
9	2093	88.8	470	10	US-09-859-053-32
10	2093	88.8	470	10	US-09-859-053-36
11	2090	88.7	451	10	US-09-822-698A-26
12	2089.5	88.7	477	12	US-10-291-265-395
13	2087.5	88.6	463	15	US-10-153-382-13
14	2083	88.4	464	15	US-10-153-382-9
15	2081.5	88.3	463	15	US-10-153-382-3

16	2081	88.3	451	15	US-10-153-382-17	Sequence 17, Appl
17	2079.5	88.2	467	12	US-10-428-408A-30	Sequence 30, Appl
18	2075.5	88.1	452	15	US-10-153-382-5	Sequence 5, Appl
19	2056.5	87.3	452	11	US-09-726-258-71	Sequence 71, Appl
20	2049	86.9	470	15	US-10-020-786-9	Sequence 9, Appl
21	2049	86.9	470	15	US-10-227-694-5	Sequence 5, Appl
22	2047	86.8	453	9	US-09-802-077-8	Sequence 8, Appl
23	2047	86.8	453	9	US-09-802-096-8	Sequence 8, Appl
24	2047	86.8	453	11	US-09-925-179-8	Sequence 8, Appl
25	2044	86.7	451	9	US-09-920-171-14	Sequence 14, Appl
26	2044	86.7	451	9	US-09-920-171-16	Sequence 16, Appl
27	2044	86.7	451	11	US-09-925-179-65	Sequence 65, Appl
28	2044	86.7	451	12	US-10-113-996-14	Sequence 14, Appl
29	2044	86.7	451	12	US-10-113-996-16	Sequence 16, Appl
30	2042.5	86.7	449	12	US-10-356-974-2	Sequence 2, Appl
31	2042.5	86.7	449	12	US-10-423-299-2	Sequence 2, Appl
32	2042.5	86.7	449	15	US-10-253-366-2	Sequence 2, Appl
33	2042.5	86.7	449	15	US-10-316-694-2	Sequence 2, Appl
34	2041	86.6	451	11	US-09-925-179-66	Sequence 66, Appl
35	2040	86.6	451	9	US-09-920-171-18	Sequence 18, Appl
36	2040	86.6	451	12	US-10-113-996-18	Sequence 18, Appl
37	2040	86.6	451	12	US-10-292-869-2	Sequence 2, Appl
38	2040	86.6	451	12	US-09-792-938-2	Sequence 2, Appl
39	2036	86.4	451	12	US-10-423-299-4	Sequence 4, Appl
40	2032	86.2	451	11	US-09-925-179-68	Sequence 68, Appl
41	2031.5	86.2	467	15	US-10-211-357-8	Sequence 8, Appl
42	2024.5	85.9	467	15	US-10-211-357-10	Sequence 10, Appl
43	2020	85.7	476	15	US-10-020-786-11	Sequence 11, Appl
44	2019.5	85.7	467	15	US-10-211-357-12	Sequence 12, Appl
45	2009.5	85.3	450	9	US-09-811-384-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-09-917-410-4
; Sequence 4, Application US/09917410
; Patent No. US20020098183A1
GENERAL INFORMATION:

APPLICANT: MARTIN, Ulrich; HASELBECK, Anton; SCHUMACHER, Guenther;

TITLE OF INVENTION: ANTI-I-SELECTIN ANTIBODIES FOR PREVENTION OF MULTIPLE ORGAN FAILURE AFTER POLYTRAUMA AND FOR PREVENTION OF ACUTE ORGAN DAMAGE AFTER EXTRACORPOREAL BLOOD CIRCULATION

NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:

ADDRESSEE: Felte & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Computer Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII, WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/917,410
FILING DATE: 26-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/578,953
FILING DATE: <Unknown>
APPLICATION NUMBER: EP 95 114 969.9
FILING DATE: 19-Sep-95
ATTORNEY/AGENT INFORMATION:

NAME: Hanson, Nc. US20020098183A1man D.
REGISTRATION NUMBER: 30 946
REFERENCE/DOCKET NUMBER: BOER 1059-PFF/NDH/SLH
TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 443
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-917-410-4

Query Match 100.0%; Score 2357; DB 9; Length 443;
Best Local Similarity 100.0%; Pred. No. 4,9e-157;
Matches 443; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMSWVRQAPGKGLEWVASISGGSTYY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMSWVRQAPGKGLEWVASISGGSTYY 60
QY 61 DSVKGRFTISRDNKNTLYIQMNSLRADETAVYYCARDYGFYDWGGTLVTVSSASTK 120
DB 61 DSVKGRFTISRDNKNTLYIQMNSLRADETAVYYCARDYGFYDWGGTLVTVSSASTK 120
QY 121 GPSVPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS 180
DB 121 GPSVPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS 180
QY 181 LSSVTVVSSSLGTITTCNVNDHKPSNTKVDKRVESKYGPPCPSPAPEFLGSPVLP 240
DB 181 LSSVTVVSSSLGTITTCNVNDHKPSNTKVDKRVESKYGPPCPSPAPEFLGSPVLP 240
QY 241 PPKKDTLMISRTPEVTCVVDVSOEDPEVQFMNYYVDGVEVNAKTKPREEOFNSTYRVS 300
DB 241 PPKKDTLMISRTPEVTCVVDVSOEDPEVQFMNYYVDGVEVNAKTKPREEOFNSTYRVS 300
QY 301 VLTIVHQMNLNGKEYKCVSNKGLPSSIEKTISSAKGQPREPOVYTLPPSQEEMTKNOVS 360
DB 301 VLTIVHQMNLNGKEYKCVSNKGLPSSIEKTISSAKGQPREPOVYTLPPSQEEMTKNOVS 360
QY 361 LTCLVKGFPYPSDIAVWESNGQPENNYKTTPPVLDSDGSFLYSRLTVDKSRWQSGNFS 420
DB 361 LTCLVKGFPYPSDIAVWESNGQPENNYKTTPPVLDSDGSFLYSRLTVDKSRWQSGNFS 420
QY 421 CSVMEALHNHYTQKSLSLGLK 443
DB 421 CSVMEALHNHYTQKSLSLGLK 443

RESULT 2
US-10-401-344-2
Sequence 2, Application US/10401344
Publication No. US20030194404A1
GENERAL INFORMATION:
APPLICANT: Schering Corporation and Abgenix, Inc.
APPLICANT: Greenfeder, Scott
APPLICANT: Corvaelan, Jose
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO INTERLEUKIN-5 AND METHODS AND COM
TITLE OF INVENTION: COMPRISING SAME
FILE REFERENCE: L101564W1
CURRENT APPLICATION NUMBER: US/10/401,344
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 465
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: STGNL
LOCATION: (1)..(19)
OTHER INFORMATION:
FEATURE:

NAME/KEY: Variable Region
LOCATION: (20)..(138)
OTHER INFORMATION:
FEATURE:
NAME/KEY: CH1 Region
LOCATION: (139)..(236)
OTHER INFORMATION:
FEATURE:
NAME/KEY: Hinge Region
LOCATION: (237)..(248)
OTHER INFORMATION:
FEATURE:
NAME/KEY: CH2 Region
LOCATION: (249)..(358)
OTHER INFORMATION:
FEATURE:
NAME/KEY: CH3 Region
LOCATION: (359)..(465)
OTHER INFORMATION:
US-10-401-344-2

Query Match 96.2%; Score 2266.5; DB 12; Length 465;
Best Local Similarity 96.4%; Pred. No. 1.1e-150;
Matches 430; Conservative 9; Mismatches 4; Indels 3; Gaps 3;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMSWVRQAPGKGLEWVASIS-TGGSTYY 59
DB 20 EVQLVESGGGLVQPGGSLRLSCAASGFTSSYAMSWVRQAPGKGLEWVSTISGGSTYY 79
QY 60 PDSYKGRFTISRDNKNTLYIQMNSLRADETAVYYCARD-YD-GYFDYWGGLTVTVSSA 117
DB 80 ADSYKGRFTISRDNKNTLYIQMNSLRADETAVYYCARDYNNVYLNHYGGLTVTVSSA 139
QY 118 STKGPSVPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 177
DB 140 STKGPSVPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 199
QY 178 LYSLSVTVVSSSLGTITTCNVNDHKPSNTKVDKRVESKYGPPCPSPAPEFLGSPV 237
DB 200 LYSLSVTVVSSSLGTITTCNVNDHKPSNTKVDKRVESKYGPPCPSPAPEFLGSPV 259
QY 238 LPPKPKDTLMISRTPEVTCVVDVSOEDPEVQFMNYYVDGVEVNAKTKPREEOFNSTYR 297
DB 260 LPPKPKDTLMISRTPEVTCVVDVSOEDPEVQFMNYYVDGVEVNAKTKPREEOFNSTYR 319
QY 298 VVSIVTVHQMNLNGKEYKCVSNKGLPSSIEKTISSAKGQPREPOVYTLPPSQEEMTKN 357
DB 320 VVSIVTVHQMNLNGKEYKCVSNKGLPSSIEKTISSAKGQPREPOVYTLPPSQEEMTKN 379
QY 358 QVSLTCLVKGFPYPSDIAVWESNGQPENNYKTTPPVLDSDGSFLYSRLTVDKSRWQSGN 417
DB 380 QVSLTCLVKGFPYPSDIAVWESNGQPENNYKTTPPVLDSDGSFLYSRLTVDKSRWQSGN 439
QY 418 VFCSCVMHEALHNHYTQKSLSLGLK 443
DB 440 VFCSCVMHEALHNHYTQKSLSLGLK 465

RESULT 3
US-10-225-108A-3
Sequence 3, Application US/10225108A
Publication No. US20030157112A1
GENERAL INFORMATION:
APPLICANT: HOOPER, Craig
APPLICANT: DIETRISCHOLD, Bernhard
TITLE OF INVENTION: Recombinant Antibodies, and Compositions
TITLE OF INVENTION: and Methods for Making Them
FILE REFERENCE: 8321-110
CURRENT APPLICATION NUMBER: US/10/225,108A
CURRENT FILING DATE: 2003-04-10
PRIOR APPLICATION NUMBER: US 09/848,832
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/204,518

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 31, 2003, 10:29:11 ; Search time 8.44244 Seconds

(without alignments)
2506.043 Million cell updates/sec

Title: US-09-917-410-5

Sequence: 1 DIQMTQSPSTLSASVGRVT.....EYTHQGLSSPVTKSFNRGEC 220

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	945.5	82.8	215	2 JE0242	Ig kappa chain NIG
2	917.5	80.3	215	2 JE0244	Ig kappa chain NIG
3	908	79.5	216	2 JE0241	Ig kappa chain Am3
4	894.5	78.3	215	2 A23746	Ig kappa chain V-I
5	891.5	78.1	215	2 JE0243	Ig kappa chain NIG
6	824	72.2	240	2 S06084	Ig kappa chain pre
7	813	71.2	214	2 S68212	Ig kappa chain (Ma
8	790	69.2	220	2 A31790	Ig kappa chain V r
9	717	62.8	230	2 S33161	Ig kappa chain - s
10	714.5	62.6	225	2 S37484	Ig kappa chain - m
11	705.5	61.8	219	2 S3865	Ig kappa chain - m
12	701.5	61.4	217	2 S42772	Ig kappa chain - m
13	699	61.2	234	2 S01320	Ig kappa chain pre
14	693.5	60.7	219	2 PC4203	Ig kappa chain (mo
15	693.5	60.7	219	2 S52028	Ig kappa chain pre
16	691.5	60.6	219	2 S16112	Ig kappa chain V r
17	685	60.0	234	2 S14237	Ig kappa chain V r
18	681	59.6	218	2 S68241	Ig kappa chain pre
19	679	59.5	218	2 JC5810	Ig kappa chain V r
20	665.5	58.3	225	2 J10029	Ig kappa chain pre
21	657.5	57.6	235	2 S25058	Ig kappa chain - m
22	649	56.8	210	2 A56169	Ig kappa chain V r
23	605	53.0	135	2 S52059	Ig kappa chain - m
24	601	52.6	178	2 A20969	Ig kappa chain V-C
25	554.5	48.0	106	1 K3HU	Ig kappa chain pre
26	548	47.2	106	1 A49633	Ig kappa chain C r
27	539.5	46.6	197	2 S29593	Ig kappa chain (W
28	532.5	44.9	99	2 A37927	Ig kappa chain C r
29	513				

30	507	44.4	99	2 S26653	Ig kappa chain C r
31	487	42.6	113	2 JC2270	pL7-6 antibody lig
32	483	42.3	109	2 S26336	Ig light chain V r
33	482	42.2	145	2 PU0014	Ig kappa chain pre
34	475	41.6	233	2 S29577	Ig light chain - r
35	474	41.5	141	2 A49134	Ig kappa chain V-I
36	472.5	41.4	145	2 S20631	Ig kappa chain - h
37	471	41.2	120	2 S51147	Ig kappa chain - h
38	470	41.2	114	1 K4HUN	antibody light cha
39	470	41.2	144	2 PU0106	Ig kappa chain V-I
40	469	41.1	127	2 S40367	Ig kappa chain pre
41	468	41.0	113	2 S34002	Ig kappa chain V-J
42	462	40.5	114	2 S44119	Ig kappa chain V r
43	461	40.4	108	2 B49047	Ig kappa chain V-J
44	460	40.3	134	2 S49531	Ig kappa chain V r
45	459	40.2	134	1 K4H017	anti-Sm antibody V
					Ig kappa chain pre

ALIGNMENTS

RESULT 1

JE0242
Ig kappa chain NIG26 precursor - human
C/Species: Homo sapiens (man)
C/Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C/Accession: JE0242
R/Alim, M.A.; Yamaki, S.; Hossein, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, submitted to JIPID, November 1998
A/Description: Structure relationship of kappa type light chains with AL amyloidosis: Mu
A/Reference number: JE0241
A/Accession: JE0242
A/Molecule type: protein
A/Residues: 1-215 <ALI>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
F,16-91/Domain: immunoglobulin homology <IMM>

Query Match 82.8%; Score 945.5; DB 2; Length 215;
Best Local Similarity 81.8%; Pred. No. 2.7e-59;
Matches 180; Conservative 17; Mismatches 18; Indels 5; Gaps 1;

QY	1	DIQMTQSPSTLSASVGRVTITKSSQSLNSNKNYLAAYOQKGAFLVYFASTR	60
DB	1	EIVLTQSPGTLSPERATLSCRASQSVN-----NYLAAYOQKGAFLVYFASTR	55
QY	61	ESGVPRFGSGSGSTDPFTLISLSLOPEDPATYFCHQHYSTPLTFGGCTKVEKRYVAAPS	120
DB	56	ATGIPRFSSGSGSTDPFTLISLSLEPEDFAVYCCQYDRPMTFGGCTKVEIRTYAAPS	115
QY	121	VFIFFPSDEQLKSGTASVCLNNFYPRKAVQWKVDNALQSGNSQESVTEQDSKDSTYS	180
DB	116	VFIFPPSDEQLKSGTASVCLNNFYPRKAVQWKVDNALQSGNSQESVTEQDSKDSTYS	175
QY	181	LSSTLTLSKADYDKHKNVACEVTHQGLSSPVTKSFNRGEC	220
DB	176	LSSTLTLSKADYDKHKNVACEVTHQGLSSPVTKSFNRGEC	215

RESULT 2

JE0244
Ig kappa chain NIG2 precursor - human
C/Species: Homo sapiens (man)
C/Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C/Accession: JE0244
R/Alim, M.A.; Hara, Y.; Hossein, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; submitted to JIPID, November 1998
A/Description: A new subgroup of kappa type light chains (VKV) identified in cases of AL am
A/Reference number: JE0243
A/Accession: JE0244
A/Molecule type: protein
A/Residues: 1-215 <ALI>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
F,16-90/Domain: immunoglobulin homology <IMM>

Query Match 80.3%; Score 917.5; DB 2; Length 215;
Best Local Similarity 81.5%; Pred. No. 2,4e-57;
Matches 181; Conservative 18; Mismatches 14; Indels 9; Gaps 4;

Qy 1 DIQMWTSPSTLSASVGDVRTITCKSSQSGLNNSNOKNYLAMYOQRGKAPKLIVYFASTR 60
Db EVLTGGPATLTVSPEGRATILSCRASGV--HSN---LAMYOQRGAOPRLLIYASTR 54

Qy 61 ESGVPDRFRTSGSGGTDPFTLTISLOPEDAFNYCHOHYST--PLTFGOGTKVEVKRTVA 118
Db ATGPAPRFSSGSGETDILTITSLSQEDPALTYIC-QQNTWPLTTGGTGKEIKRTVA 113

Qy 119 PSVFIFPPSDQLKSQTASVVCLNNFYPREAKOVKMVDNALSGNSQESVTEDSKDST 178
Db PSVFIFPPSDQLKSGTASVVCLNNFYPREAKOVKMVDNALSGNSQESVTEDSKDST 173

Qy 179 YLSISTTLTSKADYEKKHAYACEVTHOGLSSPVTKSNRGEC 220
Db YLSISTTLTSKADYEKKHAYACEVTHOGLSSPVTKSNRGEC 215

RESULT 3

JE0241 Ig kappa chain Amj3 precursor - human
C/Species: Homo sapiens (man)
C/Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C/Accession: JE0241

R.Allum, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T.
Submitted to JEPID, November 1998
A>Description: Structure relationship of kappa type light chains with AL amyloidosis. Mol
A.Reference number: JE0241
A:Accession: JE0241
A:Molecule type: protein
A:Residues: 1-216 <ALT>
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
F:16-92/Domains: immunoglobulin homology <IMM>

Query Match 79.5%; Score 908; DB 2; Length 216;
Best Local Similarity 80.9%; Pred. No. 1,1e-56;
Matches 178; Conservative 17; Mismatches 21; Indels 4; Gaps 3;

Qy 1 DIQMTPSTLSASVGDRVITTCSSQSGLNNSNOKNYLAMYQQPGAPKLIVYFASTR 60
Db 1 DIVLQGPDPIFLAVSLGERATINCKSSOSVL--YSKNFLAWYQQPGQ-PKLIIW-AANVR 56

Qy 61 ESVGPRDFRTSGSSGNDFLTITSLQPEDARYFCQHSTPLTFSGTKVEVKRTVAAPS 120
Db 57 ESVGPRDFRTSGSVGDFLTITSLNQALRYAVYYCCQYISTPSFGGRLIRKTVAAPS 116

Qy 121 VFIFPPSDQLKSQTASVVCLNNFYPREAKOVKMVDNALSGNSQESVTEDSKDSTYS 180
Db 117 VFIFPPSDQLKSQTASVVCLNNFYPREAKOVKMVDNALSGNSQESVTEDSKDSTYS 176

Qy 181 LSSTLTLSKADYEKKHAYACEVTHOGLSSPVTKSNRGEC 220
Db 177 LSSTLTLSKADYEKKHAYACEVTHOGLSSPVTKSNRGEC 216

RESULT 4

A23746 Ig kappa chain V-IIl (KAU cold agglutinin) - human
C/Species: Homo sapiens (man)
C/Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
C/Accession: A23746

R.Leoni, J.; Ghico, J.; Goni, F.; Frangione, B.
J. Biol. Chem. 265, 2836-2842, 1991
A>Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immuno-

A:Reference number: A23746; MID:91131575; PMID:1993660
A:Accession: A23746
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-215 <LEO>

Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 78.3%; Score 894.5; DB 2; Length 215;
Best Local Similarity 80.4%; Pred. No. 9,6e-56;
Matches 176; Conservative 19; Mismatches 19; Indels 5; Gaps 1;

QY 1 DIQMTGSPSTLASVGDNRVTITCKSSQSLLNSSNQKYLAMYOQKPKGAPKLLVYFASTR 60
Db 1 EIVLTGSPATLSTSPGERATLISGASQSV-----SSNYLAMYQKPEQARLLIYDASSR 55
QY 61 ESGVPDFSGSGSGTDTLTITISLQPEDFAFYFCHQHYSTPLTFGGTKVEKRTVAAPS 120
Db 56 ATGIDPDRSGSGSGTDTLTITSRLEPEDFAFYVYQYQSSPLTFGGTKVEIKRTVAAPS 115
QY 121 VFIFPPSDQIKSGTASVCLNNFYPREAKVQKVNALQSGNSQSYVTEODSKDSTYS 180
Db 116 VFIFPPSDQIKSGTASVGLNNFYPREAKVQKVNALQSGNSQSYVTEODSKDSTYS 175
QY 181 LSTLTILSKADYEKHKVYACEVTHQGLSSPPTKSFNNGE 219
Db 176 LSTLTILSKADYEKHKVYAGEVTHQGLSSPPTKSFNNGE 214

RESULT 5
JB0243
Ig kappa chain NIG93 precursor - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JB0243
R:Alim, M.A.; Hara, Y.; Hosain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.;
submitted to JPEP, November 1998
A:Description: A new subgroup of k type light chains (VKV) identified in cases of AL am
A:Reference number: JB0243
A:Molecule type: protein
A:Residues: 1-215 <ALI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 78.1%; Score 891.5; DB 2; Length 215;
Best Local Similarity 79.2%; Pred. No. 1,6e-55;
Matches 175; Conservative 18; Mismatches 21; Indels 7; Gaps 2;

QY 1 DIQMTGSPSTLASVGDNRVTITCKSSQSLLNSSNQKYLAMYOQKPKGAPKLLVYFASTR 60
Db 1 EIVMTGSPATLSTSPGERATLISCRASQSVATN-----VVMYQKLGQAPRLIILIDASSR 54
QY 61 ESGVPDRFSGSGSGTDTLTITISLQPEDFAFYFCHQHYSTPLTFGGTKVEK-RTVAAP 119
Db 55 ATGVPARFSGSGSGTDTLTITISLQSEDPATYVCGHNNAMPPTFGGTVETKRTVAAP 114
QY 120 SVFIFPPSDQIKSGTASVCLNNFYPREAKVQKVNALQSGNSQSYVTEODSKDSTY 179
Db 115 SVFIFPPSDQIKSGTASVCLNNFYPREAKVQKVNALQSGNSQSYVTEODSKDSTY 174
QY 180 SLSTLTILSKADYEKHKVYACEVTHQGLSSPPTKSFNNGEC 220
Db 175 SLSTLTILSKADYEKHKVYACEVTHQGLSSPPTKSFNNGEC 215

RESULT 6
S06084
Ig kappa chain precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
C:Accession: S06084
R:Crowe, J.S.; Smith, M.A.; Cooper, H.J.
Nucleic Acids Res 17, 7992, 1989
A:Title: Nucleotide sequence of γ 1-Ag 1.2.3, rat myeloma immunoglobulin kappa chain cDN
A:Reference number: S06084; MUID:90016888; EMD:2508067
A:Accession: S06084

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OM protein - protein search, using sw model

Run on: December 31, 2003, 10:29:10 ; Search time 5.29722 Seconds

(without alignments)
1953.078 Million cell updates/sec

Title: US-09-917-410-5

Perfect score: 1142

Sequence: 1 DIQMTQSPSTLSASVGRVT.....EYTHQGLSSPVTKSFNRGEC 220

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	548	48.0	106	KAC_HUMAN	P01834 homo sapien
2	469	41.1	114	KV4A_HUMAN	P01625 homo sapien
3	462	40.5	134	KV4C_HUMAN	P06314 homo sapien
4	445	39.0	108	KV1H_HUMAN	P01600 homo sapien
5	440.5	38.6	133	KV1B_HUMAN	P06313 homo sapien
6	435	38.1	108	KV1F_HUMAN	P01598 homo sapien
7	434	38.0	129	KV1W_HUMAN	P04431 homo sapien
8	433	37.9	108	KV1V_HUMAN	P04430 homo sapien
9	429	37.6	108	KV1M_HUMAN	P01605 homo sapien
10	426	37.3	108	KV1S_HUMAN	P01611 homo sapien
11	421	36.9	108	KV1K_HUMAN	P01603 homo sapien
12	419	36.7	108	KV1C_HUMAN	P01603 homo sapien
13	419	36.7	108	KV1R_HUMAN	P01610 homo sapien
14	417	36.5	108	KV1E_HUMAN	P01597 homo sapien
15	417	36.5	121	KV4O_HUMAN	P06312 homo sapien
16	416.5	36.5	107	KV1D_HUMAN	P01596 homo sapien
17	415	36.3	108	KV1N_HUMAN	P01596 homo sapien
18	415	36.3	109	KV4D_HUMAN	P01606 homo sapien
19	414	36.3	108	KV1N_HUMAN	P01599 homo sapien
20	414	36.3	108	KV1G_HUMAN	P01594 homo sapien
21	413	36.2	108	KV1B_HUMAN	P01607 homo sapien
22	412	36.1	108	KV1O_HUMAN	P01608 homo sapien
23	412	36.1	108	KV1V_HUMAN	P01608 homo sapien
24	406	35.6	108	KV1P_HUMAN	P01608 homo sapien
25	405.5	35.5	109	KV3D_HUMAN	P01622 homo sapien
26	405	35.5	109	KV3B_HUMAN	P01622 homo sapien
27	402.5	35.2	108	KV3L_HUMAN	P01620 homo sapien
28	401.5	34.9	129	KV1A_HUMAN	P01813 homo sapien
29	399	34.9	108	KV3M_HUMAN	P01593 homo sapien
30	398.5	34.9	139	KV3M_HUMAN	P01816 homo sapien
31	395.5	34.6	109	KV1T_HUMAN	P01612 homo sapien
32	392	34.3	129	KV1X_HUMAN	P04432 homo sapien
33	390	34.2	112	KV1U_HUMAN	P01613 homo sapien

34	390	34.2	149	1	KV5A_MOUSE	P01633 mus musculu
35	387.5	33.9	109	1	KV3E_HUMAN	P04206 homo sapien
36	386.5	33.8	109	1	KV3E_HUMAN	P01623 homo sapien
37	386	33.8	117	1	KV1U_HUMAN	P01602 homo sapien
38	383.5	33.6	109	1	KV3F_HUMAN	P01624 homo sapien
39	382	33.5	108	1	KV5D_MOUSE	P01636 mus musculu
40	379.5	33.2	108	1	KV3A_HUMAN	P01619 homo sapien
41	374	32.7	114	1	KV1A_MOUSE	P01632 mus musculu
42	372	32.6	108	1	KV5M_MOUSE	P01646 mus musculu
43	369	32.3	108	1	KV5J_MOUSE	P01643 mus musculu
44	369	32.3	117	1	KV1I_HUMAN	P01601 homo sapien
45	368.5	32.3	129	1	KV3H_HUMAN	P04207 homo sapien

ALIGNMENTS

RESULT 1
KAC_HUMAN STANDARD; PRT; 106 AA.
ID KAC_HUMAN
AC P01834;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 13-SEP-2003 (Rel. 42, Last annotation update)
DE 1g kappa chain C region.
GN IGKC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE (MYELOMA PROTEIN EU).
RX MEDLINE=71064023; PubMed=5469770;
RA Gocltieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VI. Amino
RL acid sequence of the light chain.";
RL Biochemistry 9:3155-3161(1970).
RN [2]
RP DISULFIDE BONDS.
RX MEDLINE=71064027; PubMed=4923144;
RA Gall W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.
RL Intrachain disulfide bonds.";
RL Biochemistry 9:3188-3196(1970).
RN [3]
RP SEQUENCE (BENCE-JONES PROTEIN TI).
RX MEDLINE=72186439; PubMed=5027703;
RA Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein
RT TI). IV. The complete amino acid sequence and its significance for
RL the mechanism of antibody production.";
RL Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=81042304; PubMed=6775818;
RA Hietel P.A., Max E.E., Seidman J.G., Matzel J.V., Jr., Leder P.;
RT "Cloned human and mouse kappa immunoglobulin constant and J region
RL genes conserve homology in functional segments.";
RL Cell 22:197-207(1980).
RN [5]
RP SEQUENCE (BENCE-JONES PROTEIN ROY).
RA Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,
RA Steimer-Kayne M., Suter L., Watanabe S.;
RL (in) Franek F., Shugar D. (eds.),
RL Gamma globulins: structure and function, pp.57-74, Academic Press,
RN New York (1969).
RN [6]
RP SEQUENCE (BENCE-JONES PROTEIN CUM).
RX MEDLINE=68242259; PubMed=5586923;
RA Hilschmann N.;
RT "The complete amino acid sequence of Bence Jones protein Cum (kappa-
RT type).";

RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
 [7]
 RN SEQUENCE (BENCE-JONES PROTEIN AC).
 RP MEDLINE=69234734; PubMed=4893682;
 RX Titani K., Shindoda T., Putnam F.W.;
 RA "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
 RT complete sequence and the location of the disulfide bridges";
 RL J. Biol. Chem. 244:3550-3560(1969).
 RN [8]
 RP SEQUENCE (WALDENSTROM'S MACROGLOBULIN OU).
 RX MEDLINE=70201507; PubMed=5447531;
 RA Kohler H., Shmizu A., Paul C., Putnam F.W.;
 RT "Macroglobulin structure: variable sequence of light and heavy
 chains";
 RL Science 169:56-59(1970).
 RN [9]
 RP SEQUENCE OF 1-33; 38-41 AND 62-80.
 RC TISSUE=Abdominal adipose tissue;
 RX PubMed=9586180;
 RA Olsen K.E., Sletten K., Westermarck P.;
 RT "Extended analysis of AL-amyloid protein from abdominal wall
 RL Biochem. Biophys. Res. Commun. 245:713-716(1998).
 CC -1- MISCELLANEOUS: THE EU SEQUENCE HAS THE INV (1,2) ALLOTYPIC
 CC MARKER, 45-ALA AND 83-LEU.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL: J00241; AA58989.1; -;
 DR EMBL: V00557; CA23823.1; -;
 DR PIR: B90562; K3HU.
 DR PDB: 1DSB; 09-FEB-00.
 DR PDB: 1DS1; 09-FEB-00.
 DR PDB: 1D6V; 04-OCT-00.
 DR PDB: 1HEZ; 10-AUG-01.
 DR PDB: 1HKL; 12-MAR-97.
 DR PDB: 1I7Z; 08-AUG-01.
 DR PDB: 1M1M; 15-MAY-97.
 DR Genew; HGNC:5716; IGKC.
 DR MIM: 147200; -;
 DR GO: GO:0003823; F:antigen binding activity; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003597; IG-cl.
 DR InterPro: IPR003006; IG_MHC.
 DR Pfam: PF00047; IG_1.
 DR SMART: SM00407; IGcl; 1.
 DR PROSITE: PS00290; IG_MHC; 1.
 DR Immunoglobulin domain; Immunoglobulin C region; 3D-structure.
 KW NON TER 1
 FT DOMAIN 5 102 IG-LIKE.
 FT DISULFID 26 86
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
 FT VARIANT 83 83 V->L (IN INV(1,2) MARKER).
 FT VARIANT /FTID=VAR_003897.
 FT CONFLICT 14 14 D->N (IN REF. 7 AND 8).
 FT CONFLICT 57 57 E->Q (IN REF. 5 AND 6).
 SO SEQUENCE 106 AA; 11609 MW; 51984D1FDD372C88 CRC64;
 Query Match 48.0%; Score 548; DB 1; Length 106;
 Best Local Similarity 100.0%; Pred. No. 8.6e-40;
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 115 TVAAPSVFIPPSDEQLKSGTASVYVCLINNFYPREAKVQWKVDNALQSGNSQESVTEQDS 174

Db 1 TVAAPSVFIPPSDEQLKSGTASVYVCLINNFYPREAKVQWKVDNALQSGNSQESVTEQDS 60
 Oy 175 KOSTYLSSTLTLSKADYKHYVACEVTHQGLSPVTSFNRGEC 220
 Db 61 KOSTYLSSTLTLSKADYKHYVACEVTHQGLSPVTSFNRGEC 106
 RESULT 2
 KV4A_HUMAN STANDARD; PRT; 114 AA.
 ID KV4A_HUMAN
 AC P01625;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig kappa chain V-IV region Len.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 [1]
 RP SEQUENCE.
 RX MEDLINE=76004342; PubMed=50995;
 RA Schneider M., Hilschmann N.;
 RT "The primary structure of a monoclonic immunoglobulin L-chain of
 RL subgroup IV of the kappa type (Bence-Jones protein Len).";
 RL Hoppe-Seyler's Z. Physiol. Chem. 356:507-557(1975).
 RN [2]
 RP REVISION TO 9.
 RA Salomon A.;
 RL Submitted (AUG-1996) to the SWISS-PROT data bank.
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 DR PDB: 1EEQ; 01-FEB-01.
 DR PDB: 1EEU; 03-FEB-01.
 DR PDB: 1EFQ; 03-FEB-01.
 DR PDB: 1EK3; 06-MAR-01.
 DR PDB: 1LVE; 21-JAN-98.
 DR PDB: 1LVE; 18-MAY-99.
 DR PDB: 1LVE; 28-MAR-01.
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0003823; F:antigen binding activity; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_v.
 DR Pfam: PF00047; IG_1.
 DR SMART: SM00406; IGv; 1.
 DR PROSITE: PS00835; IG_LIKE; 1.
 DR Immunoglobulin V region; Bence-Jones protein; 3D-structure.
 KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.
 FT DOMAIN 1 23
 FT DOMAIN 24 50 FRAMEWORK-1.
 FT DOMAIN 41 55 FRAMEWORK-2.
 FT DOMAIN 56 62 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 63 94 FRAMEWORK-3.
 FT DOMAIN 95 101 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 102 113 FRAMEWORK-4.
 FT DISULFID 23 94 BY SIMILARITY.
 FT NON TER 114
 SO SEQUENCE 114 AA; 12640 MW; 0647F1D17F236485 CRC64;
 Query Match 41.1%; Score 469; DB 1; Length 114;
 Best Local Similarity 76.3%; Pred. No. 4.5e-33;
 Matches 87; Conservative 13; Mismatches 14; Indels 0; Gaps 0;
 Oy 1 DIOMGSPETLSASVGRVTITCKSSQSLNNSNQNYLAWYQKRGAPKILVYFASTR 60
 Db 1 DIOMGSPETLSASVGRVTITCKSSQSLNNSNQNYLAWYQKRGAPKILVYFASTR 60
 Oy 61 ESGVDPFRFTGSGSGDTFTLTSSLOPEDPATYFCQHSHSTPLTPOGTVEVYKR 114
 Db 61 ESGVDPFRFTGSGSGDTFTLTSSLOPEDPATYFCQHSHSTPLTPOGTVEVYKR 114

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OM protein - protein search, using sw model

Run on: December 31, 2003, 10:33:16 ; Search time 22.6787 Seconds

(without alignments)
1539.764 Million cell updates/sec

Title: US-09-917-410-5

Perfect score: 1142 1 DIOMTOSPTLSASVGDRTV.....EVTHQGLSEPTKSKFNRGEC 220

Sequence: 1 DIOMTOSPTLSASVGDRTV.....EVTHQGLSEPTKSKFNRGEC 220

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_19Jun03:*

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2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*

3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*

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5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*

6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*

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8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*

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12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*

13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*

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15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*

16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*

17: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*

18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*

19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*

20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*

21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*

22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*

23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1057	92.6	242	22	AAU97949
2	1057	92.6	242	22	AAU80039
3	1057	92.6	242	22	AAU80338
4	1011	88.5	240	20	AAU50161
5	1009	88.4	214	21	AAU93735
6	1009	88.4	240	22	AAU00815
7	1007	88.2	240	23	AAE87927
8	1007	88.2	240	24	AAE82836
9	1000.5	87.6	242	20	AAU29436

10	1000.5	87.6	242	21	AAU30320	Humanised anti-IL-
11	1000.5	87.6	242	21	AAU77763	Humanised anti-IL-
12	1000.5	87.6	242	24	AAU59510	Humanised Mouse an
13	1000.5	87.6	242	24	AAU13797	Humanised mouse an
14	1000	87.6	220	18	AAU07528	Anti-HGF receptor
15	999	87.5	244	21	AAU96305	Human IGFAM-17 imm
16	998.5	87.4	242	19	AAU69302	Humanised anti-IL-
17	998.5	87.4	242	20	AAU29453	Humanised anti-IL-
18	998.5	87.4	242	21	AAU30313	Humanised anti-IL-
19	998.5	87.4	242	21	AAU77756	Humanised anti-IL-
20	998.5	87.4	242	24	AAU59503	Humanised Mouse an
21	998.5	87.4	242	24	AAU13790	Humanised mouse an
22	997.5	87.3	219	20	AAU29459	Recombinant immuno
23	997.5	87.3	219	21	AAU30323	Humanised anti-IL-
24	997.5	87.3	219	21	AAU77767	Humanised anti-IL-
25	997.5	87.3	219	24	AAU59513	Humanised Mouse an
26	997.5	87.3	219	24	AAU13800	Humanised mouse an
27	997.5	87.3	237	21	AAU963298	Human IGFAM-10 imm
28	997.5	87.3	242	19	AAU69313	Anti-IL-8 humanise
29	997.5	87.3	242	19	AAU69301	Humanised anti-IL-
30	997.5	87.3	242	20	AAU29435	Humanised anti-IL-
31	997.5	87.3	242	21	AAU30317	6G4-2-5V11N35A 11g
32	997.5	87.3	242	21	AAU77760	Humanised anti-IL-
33	997.5	87.3	242	24	AAU59507	Humanised Mouse an
34	997.5	87.3	242	24	AAU13794	Humanised mouse an
35	996	87.2	240	24	AAU38594	Hepatitis C virus
36	994.5	87.1	241	22	AAU82912	Human immune respo
37	994	87.0	260	23	AAU41164	Human ovarian anti
38	993.5	87.0	237	21	AAU96289	Human IGFAM-1 immu
39	992	86.9	363	22	AAU14228	Human novel protei
40	991	86.8	214	18	AAU34504	Light chain of hum
41	991	86.8	214	18	AAU34506	Human antibody huH
42	991	86.8	214	20	AAU08754	Humanised anti-CD1
43	991	86.8	214	20	AAU95615	Recombinant human
44	991	86.8	214	20	AAU30632	rhumAb CD18 light
45	991	86.8	214	22	AAU66777	

ALIGNMENTS

RESULT 1

AAU97949 standard; Protein; 242 AA.

AAU97949:

19-AUG-2002 (first entry)

HMFG1 FabI caspase 3 fusion construct protein #2.

Pro-caspase-3; apoptosis; cell targeting; HMFG1 FabI fusion protein;

cancer; cytotoxic; caspase.

Unidentified.

GB2360772-A.

03-OCT-2001.

28-MAR-2001; 2001GB-0007725.

28-MAR-2000; 2000GB-0007343.

(ANTI-) ANTISOMA RES LTD.

Epenetos AA;

WPI; 2001-640889/74.

N-PSDB; ABR85864.

New compounds comprising a mediator portion capable of recognising a target cell-specific molecule, and a cytotoxic portion consisting of

PT caspase, useful for treating a disease associated with the dysfunction
PT of cells, e.g. cancer -
XX
PS Examples; Fig 3; 85pp; English.

CC This invention relates to novel compounds comprising a target cell-
CC specific portion or a mediator portion capable of recognising a target
CC cell-specific molecule, and a cytotoxic portion. The compounds are
CC characterised in that the cytotoxic second portion is a constitutively
CC active caspase or has substantially the same apoptosis-inducing activity
CC as the caspases. The compounds of the invention may have cytostatic
CC activity. The compounds of the invention and compositions comprising
CC these compounds are useful in medicine, particularly useful in the
CC preparation of a medicament for treating a disease associated with the
CC dysfunction of a population of cells, such as cancer in humans. The
CC present sequence represents the HMFG1/Fab1 caspase 3 fusion protein
CC of the invention.

XX Sequence 242 AA;

Query Match 92.6%; Score 1057; DB 22; Length 242;
Best Local Similarity 92.7%; Pred. No. 1.4e-57;
Matches 204; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMTQSPSTLSASVGDRTVTITCKSSQSLNNSNQKNTLAWYQKPKAKPLLYFASTR 60
DB 23 DIQMTQSPSTLSASVGDRTVTITCKSSQSLNNSNQKNTLAWYQKPKAKPLLYFASTR 82
QY 61 ESGVDRFRITGSGSGDTFTLTSSLOPEPATYFCHQVSTPLTFQGTKEVETRTVAAPS 120
DB 83 ESGVDRFRITGSGSGDTFTLTSSLOPEPATYFCHQVSTPLTFQGTKEVETRTVAAPS 142
QY 121 VFIRPPEDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQSEVTEODSKDSTYS 180
DB 143 VFIRPPEDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQSEVTEODSKDSTYS 202
QY 181 LSTLTLSKADYEKHKYVACEVTHQGLSSPVTKSFNRGEC 220
DB 203 LSTLTLSKADYEKHKYVACEVTHQGLSSPVTKSFNRGEC 242

RESULT 2

AAU80039 standard; Protein; 242 AA.

AAU80039;

15-JUL-2002 (first entry)

HMFG1 Fab/Caspase-3 fusion protein.

Caspase-3; HMFG-1; human; milk fat globule membrane; apoptosis;
cancer; cytotoxic.

Homo sapiens.
Synthetic.

GB2360772-A.

03-OCT-2001.

28-MAR-2001; 2001GB-0007725.

28-MAR-2000; 2000GB-0007343.

(ANTI-) ANTISOMA RES LTD.

Epenetos AA;

WPI; 2001-640889/74.

N-PSDB; ABK49929.

New compounds comprising a mediator portion capable of recognising a

PT target cell-specific molecule, and a cytotoxic portion consisting of
PT caspase, useful for treating a disease associated with the dysfunction
PT of cells, e.g. cancer -
XX
PS Disclosure; Fig 3; 85pp; English.

CC The invention relates to compounds comprising a target cell-specific
CC portion or a mediator portion capable of recognising a target cell-
CC specific molecule, and a cytotoxic portion. The compounds are
CC characterised in that the cytotoxic second portion is a constitutively
CC active caspase or has substantially the same apoptosis-inducing activity
CC as the caspases. The compounds and compositions comprising the compounds
CC are useful in medicine, particularly useful in the preparation of a
CC medicament for treating a disease associated with the dysfunction of a
CC population of cells, such as cancer in a human. The present
CC sequence represents the amino acid sequence of the HMFG1 Fab/Caspase-3
CC fusion protein compound of the invention.

XX Sequence 242 AA;

Query Match 92.6%; Score 1057; DB 22; Length 242;
Best Local Similarity 92.7%; Pred. No. 1.4e-57;
Matches 204; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMTQSPSTLSASVGDRTVTITCKSSQSLNNSNQKNTLAWYQKPKAKPLLYFASTR 60
DB 23 DIQMTQSPSTLSASVGDRTVTITCKSSQSLNNSNQKNTLAWYQKPKAKPLLYFASTR 82
QY 61 ESGVDRFRITGSGSGDTFTLTSSLOPEPATYFCHQVSTPLTFQGTKEVETRTVAAPS 120
DB 83 ESGVDRFRITGSGSGDTFTLTSSLOPEPATYFCHQVSTPLTFQGTKEVETRTVAAPS 142
QY 121 VFIRPPEDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQSEVTEODSKDSTYS 180
DB 143 VFIRPPEDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQSEVTEODSKDSTYS 202
QY 181 LSTLTLSKADYEKHKYVACEVTHQGLSSPVTKSFNRGEC 220
DB 203 LSTLTLSKADYEKHKYVACEVTHQGLSSPVTKSFNRGEC 242

RESULT 3

AAU80338 standard; Protein; 242 AA.

AAU80338;

15-JUL-2002 (first entry)

Human milk fat globulin 1 (HMFG1) Fab/Caspase 1 fusion protein #2.

Human; milk fat globulin 1 Fab/Caspase 1; HMFG1; cytotoxic;
apoptosis-inducing; breast cancer; ovarian cancer; lung cancer;
stomach cancer; intestinal cancer; blood cancer; fusion protein;
tumour cell antigen.

Chimeric - Homo sapiens.
Chimeric - Synthetic.

GB2360771-A.

03-OCT-2001.

28-MAR-2000; 2000GB-0007343.

28-MAR-2000; 2000GB-0007343.

(ANTI-) ANTISOMA RES LTD.

Epenetos AA;

WPI; 2001-640888/74.

N-PSDB; ABK50713.

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 31, 2003, 10:32:16 ; Search time 17.0504 Seconds
(without alignments)
2588.856 Million cell updates/sec

Title: US-09-917-410-5

Perfect score: 1142
Sequence: 1 D1GMTSPSTLSASVGDRTV.....EYTHQGLSRVTSFNRGEC 220

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 733937 seqs, 200641211 residues

Total number of hits satisfying chosen parameters: 733937

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Published Applications AA:*
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4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1142	100.0	220	9	US-09-917-410-5
2	1057	92.6	239	10	US-09-825-012-9
3	1011	88.5	240	12	US-10-159-006-36
4	1009	88.4	214	15	US-10-153-382-19
5	1003	87.8	240	9	US-09-799-514-8
6	1000	87.6	242	11	US-10-423-299-3
7	1000	87.6	242	11	US-09-726-258-62
8	1000	87.6	220	10	US-09-895-693-1
9	998.5	87.4	220	15	US-10-232-408-1
10	997.5	87.3	242	11	US-09-726-258-51
11	997.5	87.3	219	11	US-09-726-258-72
12	994.5	87.1	242	11	US-09-726-258-56
13	992	86.9	341	15	US-10-821-945-1
14	991	86.8	363	12	US-10-291-265-335
15	991	86.8	214	9	US-09-940-166A-2

15	991	86.8	214	9	US-09-811-384-11	Sequence 11, Appl
17	991	86.8	237	9	US-09-056-160B-100	Sequence 100, App
18	991	86.8	237	9	US-09-940-166A-6	Sequence 6, Appl1
19	991	86.8	237	12	US-10-234-671-100	Sequence 100, App
20	991	86.8	237	15	US-10-020-786-10	Sequence 10, Appl
21	991	86.8	237	15	US-10-227-694-1	Sequence 1, Appl1
22	991	86.8	481	14	US-10-011-125-2	Sequence 2, Appl1
23	990	86.7	218	9	US-09-917-410-2	Sequence 2, Appl1
24	988.5	86.6	213	12	US-10-281-479A-74	Sequence 74, Appl
25	988.5	86.6	213	12	US-10-275-180A-74	Sequence 74, Appl
26	988.5	86.6	213	12	US-10-286-132A-74	Sequence 74, Appl
27	988.5	86.6	239	10	US-09-249-011A-22	Sequence 22, Appl
28	988	86.5	214	12	US-10-356-974-1	Sequence 1, Appl1
29	988	86.5	214	12	US-10-423-299-1	Sequence 1, Appl1
30	988	86.5	214	15	US-10-253-366-1	Sequence 1, Appl1
31	988	86.5	214	15	US-10-316-694-1	Sequence 1, Appl1
32	988	86.5	218	9	US-09-802-077-9	Sequence 9, Appl1
33	988	86.5	218	9	US-09-802-096-9	Sequence 9, Appl1
34	988	86.5	218	9	US-09-920-171-13	Sequence 13, Appl1
35	988	86.5	218	11	US-09-925-179-9	Sequence 9, Appl1
36	988	86.5	218	12	US-10-113-996-13	Sequence 13, Appl
37	988	86.5	220	12	US-10-159-006-17	Sequence 17, Appl
38	988	86.5	240	12	US-10-159-006-28	Sequence 28, Appl
39	985.5	86.3	213	12	US-10-281-479A-73	Sequence 73, Appl
40	985.5	86.3	213	12	US-10-275-180A-73	Sequence 73, Appl
41	985.5	86.3	213	12	US-10-320-132A-73	Sequence 73, Appl
42	984	86.2	212	12	US-10-320-132A-77	Sequence 77, Appl
43	984	86.2	216	10	US-09-859-053-30	Sequence 30, Appl
44	984	86.2	237	15	US-10-020-786-8	Sequence 8, Appl1
45	984	86.2	237	15	US-10-227-694-4	Sequence 4, Appl1

ALIGNMENTS

RESULT 1
US-09-917-410-5
Patent No. US20020098183A1
GENERAL INFORMATION:
APPLICANT: MARTIN, Ulrich; HASELBECK, Anton; SCHUMACHER, Guenther;
TITLE OF INVENTION: ANTI-L-SELECTIN ANTIBODIES FOR PREVENTION OF MULTIPLE ORGAN FAILURE AFTER POLYTRAUMA AND FOR PREVENTION OF ACUTE ORGAN DAMAGE AFTER EXTRACORPOREAL BLOOD CIRCULATION
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felte & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Computer Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII, WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/917,410
FILING DATE: 26-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/578,953
FILING DATE: <Unknown>
APPLICATION NUMBER: EP 95 114 969.9
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. US20020098183A1man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: BOER 1059-PFF/NDH/SLH
TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 688-9200
 TELEFAX: (212) 838-3884
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 220 amino acid residues
 TYPE: amino acid
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 5:
 US-09-917-410-5

Query Match 100.0%; Score 1142; DB 9; Length 220;
 Best Local Similarity 100.0%; Pred. No. 1.7e-69;
 Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSTLSASVGRVTITCKSSQSLNNSNOKNYLAWYQOKPGKAPKLLVYFASR 60
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 DB 1 DIQMTQSPSTLSASVGRVTITCKSSQSLNNSNOKNYLAWYQOKPGKAPKLLVYFASR 60
 QY 61 ESGVDRFISGSGTDFTLTISLQPEDPATYFCHQHYSTPLTFGQGTKEVVKRTVAAPS 120
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 DB 61 ESGVDRFISGSGTDFTLTISLQPEDPATYFCHQHYSTPLTFGQGTKEVVKRTVAAPS 120
 QY 121 VFIFPPSDEQLKSGTASVCLNNFYPREAKYQKVNALQSGNSQESVTEQDSKDYTS 180
 |||||
 DB 121 VFIFPPSDEQLKSGTASVCLNNFYPREAKYQKVNALQSGNSQESVTEQDSKDYTS 180
 QY 181 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 220
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 DB 181 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 220

RESULT 2

US-09-825-012-9
 ; Sequence 9, Application US/09825012
 ; Patent No. US20020122798A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Young, Robert
 ; TITLE OF INVENTION: Compounds for Targeting
 ; FILE REFERENCE: 43191-256808
 ; CURRENT APPLICATION NUMBER: US/09/825,012
 ; CURRENT FILING DATE: 2001-04-03
 ; PRIOR APPLICATION NUMBER: US 60/237,159
 ; PRIOR FILING DATE: 2000-10-02
 ; PRIOR APPLICATION NUMBER: GB 0008049.9
 ; PRIOR FILING DATE: 2000-04-03
 ; NUMBER OF SEQ ID NOS: 102
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 9
 ; LENGTH: 239
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Humanised HMF-G-1 light chain
 US-09-825-012-9

Query Match 92.6%; Score 1057; DB 10; Length 239;
 Best Local Similarity 92.7%; Pred. No. 9e-64;
 Matches 204; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMTQSPSTLSASVGRVTITCKSSQSLNNSNOKNYLAWYQOKPGKAPKLLVYFASR 60
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 DB 20 DIQMTQSPSTLSASVGRVTITCKSSQSLNNSNOKNYLAWYQOKPGKAPKLLVYFASR 79
 QY 61 ESGVDRFISGSGTDFTLTISLQPEDPATYFCHQHYSTPLTFGQGTKEVVKRTVAAPS 120
 |||||
 DB 80 ESGVDRFISGSGTDFTLTISLQPEDPATYFCHQHYSTPLTFGQGTKEVVKRTVAAPS 139
 QY 121 VFIFPPSDEQLKSGTASVCLNNFYPREAKYQKVNALQSGNSQESVTEQDSKDYTS 180
 |||||
 DB 140 VFIFPPSDEQLKSGTASVCLNNFYPREAKYQKVNALQSGNSQESVTEQDSKDYTS 199
 QY 181 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 220
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DB 200 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 229

RESULT 3

US-10-159-006-36
 ; Sequence 36, Application US/10159006
 ; Publication No. US20030143229A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Park, John E.
 ; APPLICANT: Garin-Chesa, Pilar
 ; APPLICANT: Bamberger, Uwe
 ; APPLICANT: Leger, Olivier
 ; APPLICANT: Saldanha, Jose W.
 ; APPLICANT: Rettig, Wolfgang J.
 ; TITLE OF INVENTION: FAPA-specific Antibody with Improved Productibility
 ; FILE REFERENCE: 0652.1890002
 ; CURRENT APPLICATION NUMBER: US/10/159,006
 ; CURRENT FILING DATE: 2002-06-03
 ; PRIOR APPLICATION NUMBER: US 09/301,593
 ; PRIOR FILING DATE: 1999-04-29
 ; PRIOR APPLICATION NUMBER: EP 98107925.4
 ; PRIOR FILING DATE: 1998-04-30
 ; PRIOR APPLICATION NUMBER: US 60/086,049
 ; PRIOR FILING DATE: 1998-05-18
 ; NUMBER OF SEQ ID NOS: 108
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 36
 ; LENGTH: 240
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-159-006-36

Query Match 88.5%; Score 1011; DB 12; Length 240;
 Best Local Similarity 87.7%; Pred. No. 1.1e-60;
 Matches 193; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

QY 1 DIQMTQSPSTLSASVGRVTITCKSSQSLNNSNOKNYLAWYQOKPGKAPKLLVYFASR 60
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 QY 61 ESGVDRFISGSGTDFTLTISLQPEDPATYFCHQHYSTPLTFGQGTKEVVKRTVAAPS 120
 |||||
 DB 81 ESGVDRFISGSGTDFTLTISLQPEDPATYFCHQHYSTPLTFGQGTKEVVKRTVAAPS 140
 QY 121 VFIFPPSDEQLKSGTASVCLNNFYPREAKYQKVNALQSGNSQESVTEQDSKDYTS 180
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 DB 141 VFIFPPSDEQLKSGTASVCLNNFYPREAKYQKVNALQSGNSQESVTEQDSKDYTS 200
 QY 181 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 220
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 DB 201 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 240

RESULT 4

US-10-153-382-19
 ; Sequence 19, Application US/10153382
 ; Publication No. US20030086930A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pfizer Products Inc.
 ; TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
 ; FILE REFERENCE: PC23019A
 ; CURRENT APPLICATION NUMBER: US/10/153,382
 ; CURRENT FILING DATE: 2002-05-22
 ; PRIOR APPLICATION NUMBER: 60/293042
 ; PRIOR FILING DATE: 2001-05-23
 ; NUMBER OF SEQ ID NOS: 39
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 19
 ; LENGTH: 214
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-153-382-19

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 31, 2003, 10:29:11 ; Search time 8.2769 Seconds

(without alignments)
1124.623 Million cell updates/sec

Title: US-09-917-410-5

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Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

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Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PTCUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1011	88.5	240	4 US-09-301-593-36	Sequence 36, Appl
2	1000.5	87.6	242	3 US-09-027-449-62	Sequence 62, Appl
3	1000.5	87.6	242	3 US-09-026-985-62	Sequence 62, Appl
4	1000.5	87.6	242	4 US-09-121-952A-62	Sequence 62, Appl
5	1000.5	87.6	242	4 US-09-234-340A-62	Sequence 62, Appl
6	1000	87.6	220	4 US-08-952-235-1	Sequence 1, Appl
7	1000	87.6	220	4 US-09-669-971-1	Sequence 1, Appl
8	998.5	87.4	242	3 US-09-027-449-51	Sequence 51, Appl
9	998.5	87.4	242	3 US-08-804-444A-51	Sequence 51, Appl
10	998.5	87.4	242	3 US-09-026-985-51	Sequence 51, Appl
11	998.5	87.4	242	4 US-09-121-952A-51	Sequence 51, Appl
12	998.5	87.4	242	4 US-09-234-340A-51	Sequence 51, Appl
13	997.5	87.3	219	3 US-09-027-449-72	Sequence 72, Appl
14	997.5	87.3	219	3 US-09-026-985-72	Sequence 72, Appl
15	997.5	87.3	219	4 US-09-121-952A-72	Sequence 72, Appl
16	997.5	87.3	219	4 US-09-234-340A-72	Sequence 72, Appl
17	997.5	87.3	242	3 US-09-027-449-56	Sequence 56, Appl
18	997.5	87.3	242	3 US-08-804-444A-56	Sequence 56, Appl
19	997.5	87.3	242	3 US-09-026-985-56	Sequence 56, Appl
20	997.5	87.3	242	4 US-09-121-952A-56	Sequence 56, Appl
21	997.5	87.3	242	4 US-09-234-340A-56	Sequence 56, Appl
22	996	87.2	214	2 US-07-934-373C-39	Sequence 39, Appl
23	996	87.2	214	3 US-08-437-642B-39	Sequence 39, Appl
24	996	87.2	214	5 PCT-US93-07832-39	Sequence 39, Appl
25	991	86.8	214	2 US-07-934-373C-40	Sequence 40, Appl
26	991	86.8	214	2 US-08-788-800-11	Sequence 11, Appl
27	991	86.8	214	3 US-08-437-642B-40	Sequence 40, Appl

28	991	86.8	214	3 US-09-097-309-2	Sequence 2, Appl
29	991	86.8	214	3 US-09-097-171A-2	Sequence 2, Appl
30	991	86.8	214	4 US-09-460-587-2	Sequence 2, Appl
31	991	86.8	214	5 PCT-US93-07832-40	Sequence 40, Appl
32	991	86.8	233	2 US-07-934-373C-25	Sequence 25, Appl
33	991	86.8	233	3 US-08-437-642B-25	Sequence 25, Appl
34	991	86.8	233	4 US-08-146-206C-25	Sequence 25, Appl
35	991	86.8	233	5 PCT-US93-07832-25	Sequence 25, Appl
36	991	86.8	237	3 US-09-097-309-6	Sequence 6, Appl
37	991	86.8	237	3 US-09-097-171A-10	Sequence 10, Appl
38	991	86.8	237	3 US-09-422-112B-2	Sequence 2, Appl
39	991	86.8	237	3 US-09-607-756-2	Sequence 2, Appl
40	991	86.8	237	4 US-09-460-587-6	Sequence 6, Appl
41	990	86.7	214	1 US-08-458-516-12	Sequence 12, Appl
42	990	86.7	218	5 PCT-US96-13152-2	Sequence 2, Appl
43	989.5	86.6	241	2 US-07-916-098A-56	Sequence 56, Appl
44	988	86.5	214	4 US-09-679-397-1	Sequence 1, Appl
45	988	86.5	214	4 US-09-680-148-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-301-593-36
; Sequence 36, Application US/09301593A
; Patent No. 6455677
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Legier, Olivier
; APPLICANT: Saldanha, Jose W.
; APPLICANT: Retig, Wolfgang J.
; TITLE OF INVENTION: PAP-specific Antibody with Improved Productibility
; FILE REFERENCE: 0652.1890001
; CURRENT APPLICATION NUMBER: US/09/301.593A
; EARLIER FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: EP 98107925.4
; EARLIER FILING DATE: 1998-04-30
; EARLIER APPLICATION NUMBER: US 60/086.049
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 36
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-301-593-36

Query Match 88.5%; Score 1011; DB 4; Length 240;
Best Local Similarity 87.7%; Pred. No. 7,3e-78;
Matches 193; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

QY	1	DIWMTQSPSTLSASVGDRTITTKSSQSLNNSNOKYLAWOQPKAKRLVYFASTR	60
DB	21	DIWMTQSPDLSAVSLGRATINCKSSQSLYSRNOKYLAWOQPKPKLIFMASTR	80
QY	61	ESGVPRDFSSGSGTDETLTSSLOPEDPATYCHCHYSPPLTFGQTKVEKRTVAAPS	120
DB	81	ESGVPRDFSSGSGTDETLTSSLOPEDPATYCHCHYSPPLTFGQTKVEKRTVAAPS	140
QY	121	VFIPEPDEQLKSGTASVCLNNFYPRKAVQMKVNAQSNGSSEVTEODSKDSTYS	180
DB	141	VFIPEPDEQLKSGTASVCLNNFYPRKAVQMKVNAQSNGSSEVTEODSKDSTYS	200
QY	181	LSSTLTLSKADYEKHKYACEVTHQGLSSPVTYSFNRGEC	220
DB	201	LSSTLTLSKADYEKHKYACEVTHQGLSSPVTYSFNRGEC	240

RESULT 2
US-09-027-449-62

Sequence 62, Application US/09027449
Patent No. 6025158
GENERAL INFORMATION:
APPLICANT: Gonzalez, Tania R.
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/027,449
FILING DATE: 20-Feb-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/074,330
FILING DATE: 22-Jan-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/038,664
FILING DATE: 21-Feb-1997
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R3-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 242 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-027-449-62
Query Match 87.6%; Score 1000.5; DB 3; Length 242;
Best Local Similarity 88.6%; Pred. No. 5.7e-77;
Matches 195; Conservative 8; Mismatches 16; Indels 1; Gaps 1;
QY 1 DIQMTQSPSTLSASVGDRTVITCKSSQSLNNSQNKYVLAAMYQKPKAPKLLVYFASTR 60
DB 24 DIQMTQSPSSLSASVGDRTVITCKSSQSLVHGIGF-TYLAHWQKPKAPKLLVYKXSNR 82
QY 61 ESGVDFRFGSGSGTDFLTITSSLOPEDFATYFCHQHYSTPLTFGQGTKEVEKRTVAAPS 120
DB 83 FSGVDFRFGSGSGTDFLTITSSLOPEDFATYFCHQHYSTPLTFGQGTKEVEKRTVAAPS 142
QY 121 VFIFPPSDQQLKSGTASVCLNNFYPREAKVQKVNALQSGNSQSVTEQDSKDYTS 180
DB 143 VFIFPPSDQQLKSGTASVCLNNFYPREAKVQKVNALQSGNSQSVTEQDSKDYTS 202
QY 181 LSTLTLSKADYEKHKYVACEVTHQGLSSPVTKSFNRGEC 220
DB 203 LSTLTLSKADYEKHKYVACEVTHQGLSSPVTKSFNRGEC 242

APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/026,985
FILING DATE: 20-Feb-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R3-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 242 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-026-985-62
Query Match 87.6%; Score 1000.5; DB 3; Length 242;
Best Local Similarity 88.6%; Pred. No. 5.7e-77;
Matches 195; Conservative 8; Mismatches 16; Indels 1; Gaps 1;
QY 1 DIQMTQSPSTLSASVGDRTVITCKSSQSLNNSQNKYVLAAMYQKPKAPKLLVYFASTR 60
DB 24 DIQMTQSPSSLSASVGDRTVITCKSSQSLVHGIGF-TYLAHWQKPKAPKLLVYKXSNR 82
QY 61 ESGVDFRFGSGSGTDFLTITSSLOPEDFATYFCHQHYSTPLTFGQGTKEVEKRTVAAPS 120
DB 83 FSGVDFRFGSGSGTDFLTITSSLOPEDFATYFCHQHYSTPLTFGQGTKEVEKRTVAAPS 142
QY 121 VFIFPPSDQQLKSGTASVCLNNFYPREAKVQKVNALQSGNSQSVTEQDSKDYTS 180
DB 143 VFIFPPSDQQLKSGTASVCLNNFYPREAKVQKVNALQSGNSQSVTEQDSKDYTS 202
QY 181 LSTLTLSKADYEKHKYVACEVTHQGLSSPVTKSFNRGEC 220
DB 203 LSTLTLSKADYEKHKYVACEVTHQGLSSPVTKSFNRGEC 242
RESULT 4
US-09-121-952A-62
Sequence 62, Application US/09121952A
Patent No. 6458355
GENERAL INFORMATION:
APPLICANT: Genentech, Inc., Heel, Vanessa
APPLICANT: Koumenda, Iphigenia
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
APPLICANT: Shantokh, Zahra
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 31, 2003, 10:29:11 ; Search time 17.1919 Seconds
(without alignment)
2506.043 Million cell updates/sec

Title: US-09-917-410-6

Perfect score: 2389
Sequence: 1 QVQLVQSGAEVKKPGSSVKV.....MHGALHNHYTQKSLSLSLGK 448

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR 76:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1743	73.0	327	1 G4HU	Ig gamma-4 chain C
2	1605.5	67.2	326	1 G2HU	Ig gamma-2 chain C
3	1590.5	66.6	330	1 GHHU	Ig gamma-1 chain C
4	1585	66.3	377	2 A60764	Ig gamma-3 chain C
5	1575	65.9	377	2 A23511	Ig gamma-3 chain C
6	1531	64.1	469	2 S37483	Ig gamma-2a chain C
7	1520.5	63.6	446	2 S40295	Ig gamma-2a chain C
8	1492.5	62.5	474	1 G2K811	Ig gamma-2b chain C
9	1467.5	61.4	470	2 S22080	Ig heavy chain pre
10	1448.5	60.6	472	2 S31459	Ig gamma-1 chain -
11	1433	60.0	444	2 PC4436	monoclonal antibod
12	1410	59.0	475	2 S01321	Ig gamma-2b chain C
13	1327.5	55.6	374	2 S69339	Ig heavy chain V r
14	1283.5	54.0	328	2 I47159	Ig gamma-2a chain C
15	1283.5	53.7	328	2 I47160	Ig gamma-2a chain C
16	1264.5	52.9	328	2 I47161	Ig gamma-2b chain C
17	1240.5	51.9	328	2 I47158	Ig gamma-3 chain C
18	1199	50.2	323	1 GHRB	Ig gamma-1 chain C
19	1162	48.6	329	1 G2GP	Ig gamma-2 chain C
20	1147	48.0	308	2 C30554	Ig gamma-2 chain C
21	1139.5	47.3	255	4 S31866	Ig heavy chain C r
22	1129.5	47.0	234	2 PT0207	Ig gamma-1 chain C
23	1124	46.8	326	2 PS0018	Ig gamma-2b chain C
24	1118.5	46.4	289	1 G3HWT1	Ig gamma-2b chain C
25	1108.5	46.4	329	2 S00847	Ig gamma-3 heavy C
26	1108	46.3	324	1 G1MS	Ig gamma-2c chain C
27	1106.5	46.3	330	1 G2MSA	Ig gamma-1 chain C
28	1106.5	46.3	330	1 G2MSA	Ig gamma-2a chain C
29	1103	46.2	327	2 S06611	Ig gamma-2 chain C

ALIGNMENTS

RESULT 1

G4HU

Ig gamma-4 chain C region - human

C/Species: Homo sapiens (man)

C/Date: 02-Apr-1982 #sequence revision 02-Apr-1982 #ext_change 16-Jul-1999

C/Accession: A90249; A90249; A02150

R/Elision: J.; Buxbaum, J.; Hood, L.

DNA 1, 11-18, 1981

A/Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.

A/Reference number: A90933; PMID:83157104; PMID:6299662

A/Accession: A90933

A/Molecule type: DNA

A/Residues: 1-327 <ELI>

A/Note: The sequence was determined from the germline gene

Biochem. J. 117, 33-47, 1970

A/Title: Human immunoglobulin subclones. Partial amino acid sequence of the constant

A/Reference number: A90249; PMID:70207560; PMID:4192699

A/Accession: A90249

A/Molecule type: protein

A/Residues: 1-30; 81-326 <PIN>

C/Genetics:

A/Gene: GDB:IGHG4

A/Cross-references: GDB:119340; OMIM:147130

A/Map position: 14q32.33-14q32.33

A/Introns: 99/1, 111/1, 221/1

C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap

hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into 1a

C/Superfamily: immunoglobulin C region; immunoglobulin homology

C/Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F:20-85/Domain: immunoglobulin homology <IM1>

F:134-203/Domain: immunoglobulin homology <IM2>

F:240-307/Domain: immunoglobulin homology <IM3>

F:27-83, 141-201, 247-305/Disulfide bonds: #status experimental

F:106, 109/Disulfide bonds: interchain (to heavy chain) #status experimental

F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 73.0%; Score 1743; DB 1; Length 327;

Best local similarity 100.0%; Pred. No. 26-93;

Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 122 ASTGSPVFPAPCSRSTSTALGLVVDYPPPTVWNSGALTSVHTPPAVIQSS 181

DB 1 ASTGSPVFPAPCSRSTSTALGLVVDYPPPTVWNSGALTSVHTPPAVIQSS 60

QY 182 GLVSLSSVTVPPSSSLGTTKTCNVDPKPSNTKVDKRVKSGPSPCAPFELGSPSV 241

DB 61 GLVSLSSVTVPPSSSLGTTKTCNVDPKPSNTKVDKRVKSGPSPCAPFELGSPSV 120

QY 242 PLFPPKPKDTLMISRTPEVTCVVVDVSDPEVQFNMVYDGVFNAAKTAPREBQFNSTY 301

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Db 121 FLPPKPDITMIRTEPVTCVVDVDSQEDPEVQFNMVVDGVEVHNAKTKPREQFNSTY 180
Oy 302 RVSVLTATVLDMDWLNKGYKCKVSNKGLPSSIEKTIKAKQCPPEPVYTLPSQEMTK 361
Db 181 RVSVLTATVLDMDWLNKGYKCKVSNKGLPSSIEKTIKAKQCPPEPVYTLPSQEMTK 240
Oy 362 NOVSLTCLVKGFPSPDIAVWESNGQPENNYKTPPVLDSDGSPFLYSRLTVDSKSRMQEG 421
Db 241 NOVSLTCLVKGFPSPDIAVWESNGQPENNYKTPPVLDSDGSPFLYSRLTVDSKSRMQEG 300
Oy 422 NVFSCSVHSEALHNNHYTKSLSLSGK 448
Db 301 NVFSCSVHSEALHNNHYTKSLSLSGK 327

```

RESULT 2

G2HU

Ig gamma-2 chain C region - human

C/Species: Homo sapiens (man)

C/Date: 30-Apr-1981 #sequence revision 13-Jun-1983 #ext_change 21-Jul-2000

C/Accession: A93906; A92809; A90752; A9132; A02148

R/Ellison, J.; Hood, L.

Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982

A/Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain c

A/Reference number: A93906; MUID:82197621; PMID:6804948

A/Accession: A93906

A/Molecule type: DNA

A/Residues: 1-326 <EHL>

A/Cross-references: GB:V00554; GB:J00230; NID:932759; PIDN:CA58438.1; PID:9606056

A/Note: Lys-326 is probably removed posttranslationally

R/Wang, A.C.; Tung, E.; Fudenberg, H.H.

J. Immunol. 125, 1048-1054, 1980

A/Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f

A/Reference number: A92809; MUID:81007873; PMID:6774012

A/Accession: A92809

A/Molecule type: protein

A/Residues: 1-19, 'Q', '21-57', 'Z', '59', 'A', '61-193', 'D', '195-325 <WAN>

A/Note: Trp-156 is at or near the complement-binding site

R/Connell, G.E.; Parr, D.M.; Hofmann, T.

Can. J. Biochem. 57, 758-767, 1979

A/Title: The amino acid sequences of the three heavy chain constant region domains of a

A/Reference number: A90752; MUID:8001357; PMID:113060

A/Accession: A90752

A/Molecule type: protein

A/Residues: 1-24, 'E', '26-57', 'EV', '60-85', '132-171', 'ZZZ', '175', 'B', '177-193', 'D', '195-196', 'Q', '198-

A/Note: this sequence has since been revised

R/Hofmann, T.; Parr, D.M.

Mol. Immunol. 16, 923-925, 1979

A/Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g

A/Reference number: A9132; MUID:80114419; PMID:118920

A/Accession: A9132

A/Molecule type: protein

A/Residues: 238-275 <HOF>

R/Hofmann, T.; Parr, D.M.

submitted to the Atlas, March 1980

A/Reference number: A94591

A/Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268

A/Note: the revised sequence differs from that shown in having 60-Ala and in the amidact

ned

R/Milstein, C.; Frangione, B.

Biochem. J. 121, 217-225, 1971

A/Title: Disulfide bridges of the heavy chain of human immunoglobulin G2.

A/Reference number: A90253; MUID:72033500; PMID:4940472

A/Accession: A90253

A/Molecule type: protein

A/Residues: 238-275 <HOF>

R/Hofmann, T.; Parr, D.M.

submitted to the Atlas, March 1980

A/Reference number: A94591

A/Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268

A/Note: the revised sequence differs from that shown in having 60-Ala and in the amidact

ned

R/Milstein, C.; Frangione, B.

Biochem. J. 121, 217-225, 1971

A/Title: Disulfide bridges of the heavy chain of human immunoglobulin G2.

A/Reference number: A90253; MUID:72033500; PMID:4940472

A/Accession: A90253

A/Molecule type: protein

A/Residues: 238-275 <HOF>

R/Hofmann, T.; Parr, D.M.

submitted to the Atlas, March 1980

A/Reference number: A94591

A/Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268

A/Note: the revised sequence differs from that shown in having 60-Ala and in the amidact

ned

R/Milstein, C.; Frangione, B.

Biochem. J. 121, 217-225, 1971

A/Title: Disulfide bridges of the heavy chain of human immunoglobulin G2.

A/Reference number: A90253; MUID:72033500; PMID:4940472

A/Accession: A90253

A/Molecule type: protein

A/Residues: 238-275 <HOF>

R/Hofmann, T.; Parr, D.M.

submitted to the Atlas, March 1980

A/Reference number: A94591

A/Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268

A/Note: the revised sequence differs from that shown in having 60-Ala and in the amidact

ned

R/Milstein, C.; Frangione, B.

Biochem. J. 121, 217-225, 1971

A/Title: Disulfide bridges of the heavy chain of human immunoglobulin G2.

A/Reference number: A90253; MUID:72033500; PMID:4940472

A/Accession: A90253

A/Molecule type: protein

A/Residues: 238-275 <HOF>

R/Hofmann, T.; Parr, D.M.

submitted to the Atlas, March 1980

A/Reference number: A94591

A/Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268

A/Note: the revised sequence differs from that shown in having 60-Ala and in the amidact

ned

R/Milstein, C.; Frangione, B.

Biochem. J. 121, 217-225, 1971

A/Title: Disulfide bridges of the heavy chain of human immunoglobulin G2.

A/Reference number: A90253; MUID:72033500; PMID:4940472

A/Accession: A90253

A/Molecule type: protein

A/Residues: 238-275 <HOF>

R/Hofmann, T.; Parr, D.M.

submitted to the Atlas, March 1980

A/Reference number: A94591

A/Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268

A/Note: the revised sequence differs from that shown in having 60-Ala and in the amidact

ned

R/Milstein, C.; Frangione, B.

Biochem. J. 121, 217-225, 1971

A/Title: Disulfide bridges of the heavy chain of human immunoglobulin G2.

A/Reference number: A90253; MUID:72033500; PMID:4940472

A/Accession: A90253

A/Molecule type: protein

A/Residues: 238-275 <HOF>

R/Hofmann, T.; Parr, D.M.

submitted to the Atlas, March 1980

A/Reference number: A94591

A/Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268

A/Note: the revised sequence differs from that shown in having 60-Ala and in the amidact

ned

R/Milstein, C.; Frangione, B.

Biochem. J. 121, 217-225, 1971

A/Title: Disulfide bridges of the heavy chain of human immunoglobulin G2.

A/Reference number: A90253; MUID:72033500; PMID:4940472

A/Accession: A90253

A/Molecule type: protein

A/Residues: 238-275 <HOF>

R/Hofmann, T.; Parr, D.M.

submitted to the Atlas, March 1980

A/Reference number: A94591

A/Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268

A/Note: the revised sequence differs from that shown in having 60-Ala and in the amidact

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A/Residues: 238-275 <HOF>

R/Hofmann, T.; Parr, D.M.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 31, 2003, 10:29:10 ; Search time 10.7871 Seconds
(without alignments)
1953.078 Million cell updates/sec

Title: US-09-917-410-6

Perfect score: 2389

Sequence: 1 QVQLVQSGAEVKKPGSSVKV.....MHEALHNHYTQKSLSLGK 448

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1743	73.0	327	1 GC4_HUMAN	P01661 homo sapien
2	1605.5	67.2	326	1 GC2_HUMAN	P01659 homo sapien
3	1590.5	66.6	330	1 GC1_HUMAN	P01857 homo sapien
4	1199	50.2	323	1 GC_FABIT	P01870 oryctolagus
5	1162	48.6	329	1 GC2_CAVPO	P01862 cavia porce
6	1124	47.0	333	1 GC3_RAT	P20761 rattus norv
7	1118.5	46.8	326	1 GC1_RAT	P20759 rattus norv
8	1113.5	46.6	290	1 GC3_HUMAN	P01860 homo sapien
9	1108	46.4	329	1 GC3_RAT	P20762 rattus norv
10	1106.5	46.3	324	1 GC1_MOUSE	P01868 mus musculu
11	1106.5	46.3	330	1 GC4_MOUSE	P01863 mus musculu
12	1101.5	46.1	393	1 GC1_MOUSE	P01869 mus musculu
13	1101.5	46.1	399	1 GC4_MOUSE	P01865 mus musculu
14	1099	46.0	335	1 GC4_MOUSE	P01864 mus musculu
15	1098.5	46.0	329	1 GC3_MOUSE	P22436 mus musculu
16	1090.5	45.6	398	1 GC3_MOUSE	P03987 mus musculu
17	1084.5	45.4	322	1 GC4_RAT	P20760 rattus norv
18	1054.5	44.1	336	1 GC3_MOUSE	P01866 mus musculu
19	1049.5	43.9	405	1 GC4_MOUSE	P01867 mus musculu
20	496	20.8	429	1 BPC_RAT	P01855 rattus norv
21	482.5	20.2	421	1 BPC_MOUSE	P06336 mus musculu
22	478.5	20.0	428	1 BPC_HUMAN	P01854 homo sapien
23	447.5	18.7	454	1 MUC_HUMAN	P01871 homo sapien
24	441.5	18.5	139	1 HV07_MOUSE	P01751 mus musculu
25	439	18.4	120	1 HV03_MOUSE	P01747 mus musculu
26	434.5	18.2	120	1 HV03_MOUSE	P06329 mus musculu
27	432.5	18.1	457	1 MUC_SUNMU	P20768 suncus muri
28	432.5	18.1	455	1 MUC_MOUSE	P01872 mus musculu
29	431.5	18.1	137	1 HV1_MOUSE	P01755 mus musculu
30	430.5	18.0	450	1 MUC_CANFA	P01874 canis famli
31	426	17.8	458	1 MUC_RABIT	P03988 oryctolagus
32	425	17.8	117	1 HV13_MOUSE	P01757 mus musculu
33	422.5	17.7	476	1 MUCM_MOUSE	P01873 mus musculu

34	422	17.7	454	1 MUC_MESAU	P06337 mesocricetu
35	421	17.6	117	1 HV12_MOUSE	P01756 mus musculu
36	420	17.6	140	1 HV02_MOUSE	P01746 mus musculu
37	416.5	17.4	147	1 HV1B_HUMAN	P01744 homo sapien
38	416	17.4	117	1 HV1B_HUMAN	P01743 homo sapien
39	416	17.4	479	1 MUCM_RABIT	P04221 oryctolagus
40	411.5	17.2	391	1 MUCB_HUMAN	P04220 homo sapien
41	409.5	17.1	114	1 HV00_MOUSE	P01741 mus musculu
42	406	17.0	117	1 HV1G_HUMAN	P23083 mus sapien
43	403.5	16.9	118	1 HV1I_MOUSE	P06330 mus musculu
44	402	16.8	121	1 HV01_MOUSE	P01745 mus musculu
45	397	16.6	117	1 HV1A_HUMAN	P01742 homo sapien

ALIGNMENTS

RESULT 1	GC4_HUMAN	STANDARD;	PRT;	327 AA.
AC	P01861;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	19 gamma-4 chain C region.			
GN	IGHG4.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=83157104; PubMed=6299662;			
RA	Ellison J.W., Buxbaum J.N., Hood L.E.;			
RT	"Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";			
RL	DNA 1:11-18 (1981).			
RN	(2)			
RP	SEQUENCE OF 1-30 AND 81-326.			
RX	MEDLINE=70207560; PubMed=4192699;			
RA	Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;			
RT	"Human immunoglobulin subclasses. Partial amino acid sequence of the constant region of a gamma 4 chain.";			
RL	Biochem. J. 117:33-47 (1970).			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@sib.ch).			
CC	-----			
CC	EMBL; K01316; AAB59394.1; ALT_INIT.			
DR	PIR; A90933; GAHU.			
DR	PDB; 1ADQ; 16-SEP-98.			
DR	Genew; HGNC:5528; IGHG4.			
DR	MIM; 147130.			
DR	GO; GO:0005624; C:membrane fraction; NAS.			
DR	GO; GO:0003823; F:antigen binding activity; TAS.			
DR	GO; GO:0006955; P:immune response; NAS.			
DR	InterPro; IPR007110; IG-like.			
DR	InterPro; IPR003597; IG_C1.			
DR	InterPro; IPR003006; IG_MHC.			
DR	Pfam; PF00047; I97.3.			
DR	SMART; SM00407; IG_C1.2.			
DR	PROSITE; PS50835; IG_LIKE.3.			
DR	PROSITE; PS00290; IG_MHC.2.			
KW	Immunoglobulin domain; Immunoglobulin C region; 3D-structure.			
FT	NON_TER	1		
FT	DOMAIN	1	98	CH1.
FT	DOMAIN	99	110	HINGER.
FT	DOMAIN	111	220	CH2.
FT	DOMAIN	221	327	CH3.

FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 27 83 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 141 201
 FT DISULFID 247 305
 SQ SEQUENCE 327 AA; 35940 MW; 3EDBD811EF208E7A CRC64;
 Query Match 73.0%; Score 1743; DB 1; Length 327;
 Best Local Similarity 100.0%; Pred. No. 1,1e-111; Indels 0; Gaps 0;
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 122 ASTKGPEVFLPAPCSRSTSESTALGCLVNDYFPEPTVSNNGALTSVHTPPAVLQSS 181
 1 ASTKGPEVFLPAPCSRSTSESTALGCLVNDYFPEPTVSNNGALTSVHTPPAVLQSS 60
 DB 182 GLVSLSSVTVYPSSSSLGKTYTTCNVDPKPSNTKDKVESKYGPPCGSCAPFLGPPSV 241
 61 GLVSLSSVTVYPSSSSLGKTYTTCNVDPKPSNTKDKVESKYGPPCGSCAPFLGPPSV 120
 QY 242 FLPPPKRDTLMISRTPEVTCVVVDVSOEDPEVQFNMYVDGVEVHNAKTKPREEQFNSTY 301
 121 FLPPPKRDTLMISRTPEVTCVVVDVSOEDPEVQFNMYVDGVEVHNAKTKPREEQFNSTY 180
 DB 302 RVSVSVLTVLHQDWLNGKYEKCKVSNKGLPSSIEKTIISKAKQPREPOVYTLPSQSEMTK 361
 181 RVSVSVLTVLHQDWLNGKYEKCKVSNKGLPSSIEKTIISKAKQPREPOVYTLPSQSEMTK 240
 QY 362 NVQSVLTCLVKGFPYPSDIAVWESNNGQPPNNYKTPPYLDSDGSEFFLYSRLTVDKSRWQEG 421
 241 NVQSVLTCLVKGFPYPSDIAVWESNNGQPPNNYKTPPYLDSDGSEFFLYSRLTVDKSRWQEG 300
 QY 422 NVFSCSVMEALHNHYTQKSLSLGK 448
 301 NVFSCSVMEALHNHYTQKSLSLGK 327
 DB
 RESULT 2
 GC2_HUMAN STANDARD; PRT; 326 AA.
 AC P01859;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE IG gamma-2 chain C region.
 GN IGHG2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE OF 2-326 FROM N.A.
 RA MEDLINE=82197621; PubMed=6804948;
 RA Ellison J.W., Hood L.E.;
 RT "Linkage and sequence homology of two human immunoglobulin gamma
 heavy chain constant region genes."
 RL Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).
 RN [2]
 RP SEQUENCE OF 88-115 FROM N.A.
 RC TISSUE=Fetal liver;
 RX MEDLINE=83001943; PubMed=6811139;
 RA Takahashi N., Ueda S., Obata M., Nikaido T., Nakai S., Honjo T.;
 RT "Structure of a human immunoglobulin gamma genes: implications for
 evolution of a gene family."
 RL Cell 29:671-679(1982).
 RN [3]
 RP SEQUENCE OF 99-177 AND 310-326 FROM N.A.
 RC TISSUE=Fetal liver;
 RX MEDLINE=84235992; PubMed=6329676;
 RA Krawinkel U., Rabbitts T.H.;
 RT "Comparison of the hinge-coding segments in human immunoglobulin gamma
 heavy chain genes and the linkage of the gamma 2 and gamma 4 subclasses
 genes.";

RL EMBO J. 1:403-407(1982).
 RN [4]
 RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
 RX MEDLINE=81007873; PubMed=6774012;
 RA Wang A.-C., Tung E., Fudenberg H.H.;
 RT "The primary structure of a human IgG2 heavy chain: genetic,
 evolutionary, and functional implications."
 RL J. Immunol. 125:1048-1054(1980).
 RN [5]
 RP SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
 RX MEDLINE=8001357; PubMed=113060;
 RA Connell G.E., Parr D.M., Hofmann T.;
 RT "The amino acid sequences of the three heavy chain constant region
 domains of a human IgG2 myeloma protein."
 RL Can. J. Biochem. 57:758-767(1979).
 RN [6]
 RP SEQUENCE OF 238-275 (ZIE).
 RX MEDLINE=80114419; PubMed=118920;
 RA Hofmann T., Parr D.M.;
 RT "A note of the amino acid sequence of residues 381-391 of human
 immunoglobulin gamma chains."
 RL Mol. Immunol. 16:923-925(1979).
 RN [7]
 RP REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
 RA Hofmann T., Parr D.M.;
 RL Submitted (MAR-1980) to the PIR data bank.
 RN [8]
 RP SEQUENCE OF 1-121 (DOT).
 RX MEDLINE=95255298; PubMed=7737190;
 RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
 RT "Characterization of the two unique human anti-flavon monoclonal
 immunoglobulins."
 RL Eur. J. Biochem. 228:886-893(1995).
 RN [9]
 RP DISULFIDE BONDS.
 RX MEDLINE=72033500; PubMed=4940472;
 RA Miletic C., Frangione B.;
 RT "Disulphide bridges of the heavy chain of human immunoglobulin G2."
 RL Biochem. J. 121:217-225(1971).
 RN [10]
 RP DISULFIDE BONDS.
 RX MEDLINE=69064124; PubMed=5782707;
 RA Frangione B., Miletic C., Pink J.R.L.;
 RT "Structural studies of immunoglobulin G."
 RL Nature 221:145-148(1969).
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 CC EMBL; J00230; AAB59393.1; -.
 DR PIR; A93906; G2HU.
 DR HSSP; P01857; 1FC1.
 DR Genew; HGNC:5526; IGHG2.
 DR MTM; 147110; -.
 DR GO; GO:0005624; C:membrane fraction; NAS.
 DR GO; GO:0003823; F:antigen binding activity; TAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_C1.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00407; IgC1; 2.
 DR PROSITE; PS00835; IG_LIKE; 3.
 DR PROSITE; PS00290; IG_MHC; 2.
 KM Immunoglobulin domain; Immunoglobulin C region.
 FT NON_TER 1 1
 FT DOMAIN 1 98 CH1.
 FT DOMAIN 99 110 HINGE.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 31, 2003, 10:29:10 ; Search time 38.0918 Seconds
(without alignments)
3034.973 Million cell updates/sec

Title: US-09-917-410-6

Perfect score: 2389
Sequence: 1 QVQLVQSGAEVKKPGSSVKRV.....MHEALHNYTKSLSLGK 448

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp Unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1982.5	83.0	473	4	Q8TC63
2	1948	81.5	471	4	Q8TC77
3	1896	79.4	521	4	Q8N4Y9
4	1571	65.8	509	4	Q8N617
5	1538	64.4	473	11	Q9B8L4
6	1535	64.3	463	11	Q991C4
7	1531	64.1	473	11	Q991Z5
8	1483.5	62.1	468	11	Q991J1
9	1451	60.7	469	11	Q8R3V9
10	1432.5	60.0	474	11	Q8R3H6
11	1428	59.8	437	11	Q9R1A4
12	1409	59.0	473	11	Q91Z05
13	1217	50.9	337	6	Q95M34
14	1139.5	47.7	701	4	Q96P08
15	901	37.7	614	4	Q96GA6
16	842.5	35.3	613	11	Q8VCX7

17	833.5	34.9	278	11	Q921K1	Q921K1 mus musculus
18	815.5	34.1	503	4	Q8WUX1	Q8WUX1 homo sapien
19	812.5	34.0	500	4	Q9BVR0	Q9BVR0 homo sapien
20	807	33.8	597	4	Q96BB9	Q96BB9 homo sapien
21	791	33.1	481	11	Q91WR1	Q91WR1 mus musculus
22	787	32.9	497	4	Q8WY24	Q8WY24 homo sapien
23	784.5	32.8	482	11	Q8K172	Q8K172 mus musculus
24	766	32.1	481	11	Q8VCV5	Q8VCV5 mus musculus
25	762	31.9	489	11	Q8VCX4	Q8VCX4 mus musculus
26	760.5	31.8	488	11	Q8K0F2	Q8K0F2 mus musculus
27	750.5	31.8	496	4	Q96DK0	Q96DK0 homo sapien
28	759.5	31.8	480	11	Q8K0Z4	Q8K0Z4 mus musculus
29	756	31.6	493	4	Q8NCL6	Q8NCL6 homo sapien
30	755.5	31.6	488	11	Q91WR1	Q91WR1 mus musculus
31	742.5	31.1	494	4	Q96K68	Q96K68 homo sapien
32	735	30.8	481	11	Q91WT3	Q91WT3 mus musculus
33	734	30.7	597	4	Q9BUI0	Q9BUI0 homo sapien
34	730	30.6	597	4	Q9BQB8	Q9BQB8 homo sapien
35	727.5	30.5	484	11	Q991A6	Q991A6 mus musculus
36	724	30.3	618	4	Q8WUX4	Q8WUX4 homo sapien
37	724	30.3	618	4	Q96A66	Q96A66 homo sapien
38	722	30.2	487	11	Q99KA4	Q99KA4 mus musculus
39	715.5	29.9	613	4	Q96EY0	Q96EY0 homo sapien
40	712	29.8	499	4	Q8N5K4	Q8N5K4 homo sapien
41	696.5	29.2	486	11	Q91Z07	Q91Z07 mus musculus
42	693	29.0	479	11	Q91WP5	Q91WP5 mus musculus
43	687.5	28.8	484	11	Q8VEA0	Q8VEA0 mus musculus
44	668	28.0	480	11	Q91XE1	Q91XE1 mus musculus
45	658.5	27.6	482	11	Q91X92	Q91X92 mus musculus

ALIGNMENTS

RESULT 1

ID Q8TC63 PRELIMINARY; PRT; 473 AA.
AC Q8TC63;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; BC025985; AAH25985.1;
DR InterPro; IPR000923; Bluecu_1.
DR InterPro; IPR007110; IG-1-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_4.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS00196; COPPER_BLUE; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;

Query Match 83.0%; Score 1982.5; DB 4; Length 473;
Best Local Similarity 84.3%; Pred. No. 1.1e-162;
Matches 380; Conservative 24; Mismatches 40; Indels 7; Gaps 4;

QY 1 QVQLVQSGAEVKKPGSSVKASG--YTFPSYVMHWROAPGGGLMIGIYYPNGT 58
DB 27 RIQLQSGEGLIKPEVITSLTCTVSGDSVASSSYTWGVRQPPGKGLMIGIT-NFSGNM 85
QY 59 KNEKFKGRVITSDSTNTAYMELSLRSDTAVYGCAREYGNVYFVDF-WGQGTIV 117

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Db      86  YSPSLRSRTVMSADMSNSFYLTLDSTVADTAADYVCAA---GHLMGFGAHMGQGLV 142
Qy      118 TVSSASTKGPSVFPLAACSSTGSESTAALGCLVKDYFPEPVTVSNMGSALTSGVHPFPAV 177
Db      143 SVSPASASTKGPSVFPLAACSSTGSESTAALGCLVDYFPEPVTVSNMGSALTSGVHPFPAV 202
Qy      178 LOSGGLSLSSVTVFPSSSLGTCTYTCNVDPHKPSNTKYDKRVESKYGPSPGPSAPAEFLG 237
Db      203 LOSGGLSLSSVTVFPSSSLGTCTYTCNVDPHKPSNTKYDKRVESKYGPSPGPSAPAEFLG 262
Qy      238 GPSVFLEPPPKDITLMSRTPEVTCVVVDVSDPEVFQFMWYDGVENNAKTKPREEQF 297
Db      263 GPSVFLEPPPKDITLMSRTPEVTCVVVDVSDPEVFQFMWYDGVENNAKTKPREEQF 322
Qy      298 NSTYRVSVTLTVLHODMUNGKEYCKVSNKGLPSSIEKTSKAAGPREPQVTLPSQOE 357
Db      323 NSTYRVSVTLTVLHODMUNGKEYCKVSNKGLPSSIEKTSKAAGPREPQVTLPSQOE 382
Qy      358 EMTKNQVSLTCLVKGFPSPDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSRLTVDKSR 417
Db      383 EMTKNQVSLTCLVKGFPSPDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSRLTVDKSR 442
Qy      418 WQEGNVFSCSVMEHALHNHTOKSLSLSLGK 448
Db      443 WQEGNVFSCSVMEHALHNHTOKSLSLSLGK 473

RESULT 2
Q8TC77  PRELIMINARY; PRT; 471 AA.
ID      Q8TC77;
AC      Q8TC77;
DT      01-JUN-2002 (Tremblrel. 21, Created)
DT      01-JUN-2002 (Tremblrel. 21, last sequence update)
DT      01-MAR-2003 (Tremblrel. 23, last annotation update)
DE      Hypothetical protein.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Spleen;
RA      Strauberg R.;
RL      Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR      EMBL; BC024289; AAH24289.1; -.
DR      InterPro; IPR007110; IG_1like.
DR      InterPro; IPR003006; IG_MHC.
DR      InterPro; IPR003596; IG_V.
DR      Pfam; PF00047; IG_4.
DR      SMART; SM00406; IGV; 1.
DR      PROSITE; PSS0835; IG_LIKE; 4.
DR      PROSITE; PSS00290; IG_MHC; 2.
KW      Hypothetical protein.
SQ      SEQUENCE 471 AA; 51791 MW; 388F7F4CF58866DE CRC64;

Query Match      81.5%; Score 1948; DB 4; Length 471;
Best Local Similarity 80.4%; Pred. No. 1e-159;
Matches 370; Conservative 37; Mismatches 33; Indels 20; Gaps 5;

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Db      192 HFFPALQSSGLYSLSSVTVFPSSSLGTCTYTCNVDPHKPSNTKYDKRVESKYGPSPGPSAPAEFLG 251
Qy      229 SCPAPAEFLGSPSVFLFPPPKDITLMSRTPEVTCVVVDVSDPEVFQFMWYDGVENNA 288
Db      252 PCPAPAEFLGSPSVFLFPPPKDITLMSRTPEVTCVVVDVSHDPEVQFMWYDGVENNA 311
Qy      289 KTKPREEQNSTYRVSVTLTVLHODMUNGKEYCKVSNKGLPSSIEKTSKAAGPREPQ 348
Db      312 KTKPREEQNSTYRVSVTLTVLHODMUNGKEYCKVSNKGLPSSIEKTSKAAGPREPQ 371
Qy      349 VYTLPSQOEMTKNQVSLTCLVKGFPSPDIAVEMESNGQPENNYKTPPVLDSDGSFFLY 408
Db      372 VYTLPSQOEMTKNQVSLTCLVKGFPSPDIAVEMESNGQPENNYKTPPVLDSDGSFFLY 431
Qy      409 SRLTVDKSRWQEGNVFSCSVMEHALHNHTOKSLSLSLGK 448
Db      432 SKLTVDKSRWQEGNVFSCSVMEHALHNHTOKSLSLSLGK 471

RESULT 3
Q8N4Y9  PRELIMINARY; PRT; 521 AA.
ID      Q8N4Y9;
AC      Q8N4Y9;
DT      01-OCT-2002 (Tremblrel. 22, Created)
DT      01-OCT-2002 (Tremblrel. 22, last sequence update)
DT      01-MAR-2003 (Tremblrel. 23, last annotation update)
DE      Hypothetical protein.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Primary B-Cells from Tonsils;
RA      Strauberg R.;
RL      Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR      EMBL; BC033178; AAH33178.1; -.
DR      InterPro; IPR007110; IG_1like.
DR      InterPro; IPR003597; IG_C1.
DR      InterPro; IPR003006; IG_MHC.
DR      InterPro; IPR003596; IG_V.
DR      Pfam; PF00047; IG_4.
DR      SMART; SM00407; IGV; 3.
DR      SMART; SM00406; IGV; 1.
DR      PROSITE; PSS0835; IG_LIKE; 4.
DR      PROSITE; PSS00290; IG_MHC; 2.
KW      Hypothetical protein.
SQ      SEQUENCE 521 AA; 57156 MW; 2AC7D22872D6CAA2 CRC64;

Query Match      79.4%; Score 1896; DB 4; Length 521;
Best Local Similarity 71.9%; Pred. No. 3.7e-155;
Matches 361; Conservative 37; Mismatches 50; Indels 54; Gaps 3;

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OM protein - protein search, using sw model

Run on: December 31, 2003, 10:33:16 ; Search time 46.1821 Seconds

(without alignments)
1539.764 Million cell updates/sec

Title: US-09-917-410-6

Perfect score: 2389

Sequence: 1 QVQLVSGAIVKRPSSVKV.....MHBALNHYTKLSLSLQK 448

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	2265.5	94.8	AA28808	pre-5A8 humanised
2	2162.5	90.5	AAW14941	3F4 Human IgG4 exp
3	2162.5	90.5	AAW14938	Murine anti-porcine
4	2159.5	90.4	AAW14935	Humanised 323/A3 (
5	2153.5	90.1	AAW14935	Humanised 323/A3 (
6	2121	88.8	AAW14935	2A2 Human IgG4 exp
7	2121	88.8	AAW14932	Murine anti-porcine
8	2111	88.4	AAW14932	Anti-human IL-4 hu
9	2106.5	88.2	AAW13564	Humanised anti-L-s

10	2101.5	88.0	449	14	AA433339	Completely humanis
11	2101.5	88.0	449	19	AAW49816	Amino acid sequenc
12	2098.5	87.8	447	18	AAW10232	TF8-5G9 CDR-graite
13	2093.5	87.6	470	21	AAW90936	Humanised HFE7A de
14	2093.5	87.6	470	23	ABW74945	Humanised anti-Fas
15	2093.5	87.6	470	23	AAU74296	Anti-human ALLIM m
16	2086.5	87.3	470	21	AAW90935	Humanised anti-Fas
17	2086.5	87.3	470	23	ABW74904	Mouse humanised an
18	2085.5	87.3	470	21	AAW90934	Humanised anti-Fas
19	2085.5	87.3	470	23	ABW74903	Mouse humanised an
20	2083.5	87.2	470	21	AAW90933	Humanised anti-Fas
21	2083.5	87.2	470	23	ABW74902	Humanised anti-Fas
22	2082.5	87.2	472	23	ABP51695	5G1.1-TPO heavy ch
23	2080.5	87.1	470	19	AAW83037	Anti-Fas humanised
24	2080.5	87.1	470	21	AAW14779	Humanised anti-Fas
25	2080.5	87.1	470	21	AAW90929	Humanised HFE7A de
26	2080.5	87.1	470	23	ABW74898	Humanised anti-Fas
27	2080.5	87.1	470	23	ABW74944	Humanised anti-Fas
28	2079	87.0	448	23	ABW99224	Chimeric CD45RO/RB
29	2077	86.9	583	22	AAW83156	Ganglioside GM2 an
30	2069.5	86.6	652	19	AAW48650	Heavy chain of hMA
31	2069	86.6	463	18	AAW14939	3F4 (Chimeric) hum
32	2069	86.6	463	18	AAW14940	3F4 (Chimeric) hum
33	2067.5	86.5	470	19	AAW83036	Anti-Fas humanised
34	2067.5	86.5	470	21	AAW14776	Humanised anti-Fas
35	2067.5	86.5	470	21	AAW90926	Humanised HFE7A de
36	2067.5	86.5	470	23	ABW74895	Humanised anti-Fas
37	2067.5	86.5	470	23	ABW74941	Humanised anti-Fas
38	2061	86.3	731	22	AAW52156	Humanised HMFg-1 h
39	2061	86.3	741	22	AAW52159	Humanised HMFg-1 h
40	2056	86.1	729	22	AAW52158	Humanised HMFg-1 h
41	2056	86.1	729	22	AAW52161	Humanised HMFg-1 h
42	2053	85.9	730	22	AAW52157	Humanised HMFg-1 h
43	2053	85.9	740	22	AAW52160	Humanised HMFg-1 h
44	2051	85.9	461	22	ABW72236	Humanised 323/A3 (
45	2050.5	85.8	476	24	ABU08022	Monoclonal rabies

ALIGNMENTS

RESULT 1	
AA28808	AA28808 standard; Protein; 468 AA.
ID	
AA28808	
AC	AA28808;
XX	
DT	25-MAR-2003 (updated)
DT	02-APR-1993 (first entry)
XX	
DE	pre-5A8 humanised heavy chain.
XX	
KW	Vector: PMDR1002; Noct; HindIII; PMDR1001; pSAB132; pSAB101; E. coli;
KW	UA221(Ig); ampicillin; resistance; immunoglobulin; signal sequence;
KW	humanised; 5A8; heavy chain; variable; region; HV; IgG4; constant;
KW	HC; antibody; homolog; CD4; gp120; cell surface glycoprotein; CD4+;
KW	lymphocytes; helper; inducer; HIV; syncytia; formation.
XX	
OS	Synthetic.
XX	
Key	Location/Qualifiers
FT	1..19
FT	/note= "Immunoglobulin signal peptide"
FT	20..141
FT	/note= "Humanised 5A8 HV"
FT	142..468
FT	/note= "Human IgG4 HC"
XX	
PN	W09209305-A1.
XX	
PD	11-JUN-1992.
XX	
PF	27-NOV-1991; 91WO-US08843.

XX 27-NOV-1990; 90US-0618542.
 XX (BIOF) BIOGEN INC.
 XX
 XX Burkly LC, Chisholm PL, Rosa JT, Rosa MD, Thomas DW;
 XX WPI; 1992-398399/48.
 XX DR N-PSDB; AAQ30910.
 XX
 PT New anti-CD4 antibody homologues - which bind CD4, do not block
 PT binding of HIV gp120 to CD4 but block HIV-induced syncytia
 PT formation between CD4+ cells
 XX
 XX Disclosure; Page 155-56; 205pp; English.
 XX
 CC This sequence is encoded by the insert of the vector pMDR1002. Three
 CC fragments were used in the construction of pMDR1002; a 443 bp NotI/
 CC HindIII fragment of pMDR1001 (see AAQ30905), the 7913 bp NotI linearised
 CC pSAB132 (see AAQ30906) and a 2109 bp NotI/HindIII fragment of pBAG101
 CC (see AAQ30909). These fragments were ligated together and the ligation
 CC mixture was used to transform E. coli JA221(Ig) to ampicillin
 CC resistance. This sequence represents the immunoglobulin signal
 CC sequence, amino acids (AA) 1-122 of the humanised 5A8 heavy chain
 CC variable region (HV) and AA114-AA478 of the human IgG4 heavy chain,
 CC ie, the constant region (HC). This polypeptide is an antibody homolog
 CC which was shown to bind to CD4 but did not block the binding of gp120
 CC to CD4. CD4 is a cell surface glycoprotein of CD4+ lymphocytes
 CC (helper/inducer cells). The homolog blocked HIV-induced syncytia
 CC formation. This homolog can be used in the detection, prophylaxis
 CC and treatment of diseases caused by infective agents whose primary
 CC targets are CD4+ cells.
 CC (Updated on 25-MAR-2003 to correct FN field.)
 CC
 XX Sequence 468 AA;
 SQ
 Query Match 94.8%; Score 2265.5; DB 13; Length 468;
 Best Local Similarity 95.1%; Pred. No. 5.5e-13;
 Matches 428; Conservative 8; Mismatches 11; Indels 3; Gaps 2;

RESULT 2
 AAW14941
 ID AAW14941 standard; Protein; 464 AA.
 XX
 XX AAW14941;
 AC
 XX
 XX 16-JUN-1997 (first entry)
 DT
 XX
 XX 3F4 Human IgG4 expression plasmid insert product (heavy chain).
 DE
 XX
 KW Xenotransplantation; graft rejection; cell interaction; pig;
 KW vascular cell adhesion molecule; VCAM; monoclonal antibody;
 KW chimeric antibody; diagnosis.
 KM
 XX
 OS Mus sp.
 OS
 XX
 XX WO9711971-A1.
 PN
 XX
 XX 03-APR-1997.
 PD
 XX
 XX 27-SEP-1996; 96WO-US15575.
 PF
 XX
 XX 26-SEP-1996; 96US-0004489.
 PR
 XX 28-SEP-1995; 95US-0004489.
 XX
 XX (ALEX-) ALEXION PHARM INC.
 PA
 XX
 XX Evans MJ, Matie LA, Mueller EE, Mueller JP, Rollins S;
 PI
 XX
 XX Rother RP;
 DR
 XX WPI; 1997-212855/19.
 DR
 XX N-PSDB; AAT62938.
 XX
 PT Antibodies binding to porcine but not human cell interaction
 PT proteins - useful to treat and assay for rejection of xenografted
 PT porcine organs, tissues or cells
 PT
 XX
 XX Disclosure; Page 62-64; 105pp; English.
 CC
 CC Heavy chain (AAW14941) and light chain (AAW14942) sequences
 CC correspond to murine anti-porcine soluble vascular cell adhesion
 CC molecule (VCAM) monoclonal antibody 3F4 (see also AAW14937-38). They
 CC are encoded by a 3F4 human IgG4 expression plasmid insert (see
 CC also AAT62938). A chimeric antibody specific for porcine VCAM can be
 CC produced in transfected host cells. It is useful for diagnosing
 CC human rejection of porcine xenotransplants and for improving
 CC xenotransplantation of porcine cells, tissues and organs into human
 CC recipients.
 CC
 XX Sequence 464 AA;
 SQ
 Query Match 90.5%; Score 2162.5; DB 18; Length 464;
 Best Local Similarity 90.4%; Pred. No. 1.1e-124;
 Matches 405; Conservative 18; Mismatches 22; Indels 3; Gaps 1;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 31, 2003, 10:32:16 ; Search time 34.7208 Seconds

(without alignments)
2588.856 Million cell updates/sec

Title: US-09-917-410-6

Perfect score: 2389
1 QVQLVSGAIVKRGSSVKV.....MHEALHNYTKSLSLSLGK 448

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 733937 seqs, 200641211 residues

Total number of hits satisfying chosen parameters: 733937

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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18: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2389	100.0	448	9	US-09-917-410-6
2	2226	93.2	467	12	US-10-428-408A-30
3	2115	88.5	465	12	US-10-401-344-2
4	2106.5	88.2	443	9	US-09-917-410-4
5	2093.5	87.6	470	10	US-09-859-053-28
6	2093.5	87.6	470	12	US-10-384-933-157
7	2093.5	87.6	470	15	US-10-384-484-157
8	2086.5	87.3	470	12	US-10-384-933-147
9	2086.5	87.3	470	15	US-10-384-484-147
10	2085.5	87.3	470	12	US-10-384-933-145
11	2085.5	87.3	470	15	US-10-384-484-145
12	2083.5	87.2	470	12	US-10-384-933-143
13	2083.5	87.2	470	15	US-10-384-484-143
14	2082.5	87.2	472	12	US-10-307-724-67
15	2082.5	87.2	472	15	US-10-006-593-67

16	2081	87.1	461	10	US-09-249-011A-24	Sequence 24, Appl
17	2080.5	87.1	470	12	US-10-384-933-117	Sequence 117, App
18	2080.5	87.1	470	15	US-10-216-484-117	Sequence 117, App
19	2067.5	86.5	470	12	US-10-384-933-89	Sequence 89, Appl
20	2067.5	86.5	470	15	US-10-216-484-89	Sequence 89, Appl
21	2061	86.3	731	10	US-09-825-012-46	Sequence 46, Appl
22	2061	86.3	741	10	US-09-825-012-55	Sequence 55, Appl
23	2059	86.2	448	12	US-10-353-708-48	Sequence 48, Appl
24	2059	86.2	448	12	US-10-353-708-60	Sequence 60, Appl
25	2059	86.2	448	15	US-10-171-452A-48	Sequence 48, Appl
26	2059	86.2	448	15	US-10-171-452A-60	Sequence 60, Appl
27	2059	86.2	467	12	US-10-353-708-41	Sequence 41, Appl
28	2059	86.2	467	12	US-10-353-708-47	Sequence 47, Appl
29	2059	86.2	467	12	US-10-353-708-59	Sequence 59, Appl
30	2059	86.2	467	15	US-10-171-452A-41	Sequence 41, Appl
31	2059	86.2	467	15	US-10-171-452A-47	Sequence 47, Appl
32	2059	86.2	467	15	US-10-171-452A-59	Sequence 59, Appl
33	2056	86.1	448	12	US-10-353-708-42	Sequence 42, Appl
34	2056	86.1	448	12	US-10-353-708-54	Sequence 54, Appl
35	2056	86.1	448	15	US-10-171-452A-42	Sequence 42, Appl
36	2056	86.1	448	15	US-10-171-452A-54	Sequence 54, Appl
37	2056	86.1	467	12	US-10-353-708-53	Sequence 53, Appl
38	2056	86.1	467	15	US-10-171-452A-53	Sequence 53, Appl
39	2056	86.1	729	10	US-09-825-012-52	Sequence 52, Appl
40	2056	86.1	729	10	US-09-825-012-61	Sequence 61, Appl
41	2053	85.9	730	10	US-09-825-012-49	Sequence 49, Appl
42	2053	85.9	740	10	US-09-825-012-58	Sequence 58, Appl
43	2050.5	85.8	476	12	US-10-225-108A-16	Sequence 16, Appl
44	2033	85.1	452	11	US-09-726-258-71	Sequence 71, Appl
45	2026.5	84.8	476	10	US-09-747-669-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-09-917-410-6
Sequence 6, Application US/09917410
Patent No. US20020098183A1

GENERAL INFORMATION:
APPLICANT: MARTIN, Ulrich; HASSELBECK, Anton; SCHUMACHER, Guenther;
CO, Man S.
TITLE OF INVENTION: ANTI-L-SELECTIN ANTIBODIES FOR PREVENTION OF MULTIPLE ORGAN FAILURE AFTER POLYTRAUMA AND FOR PREVENTION OF ACUTE ORGAN DAMAGE AFTER EXTRACORPOREAL BLOOD CIRCULATION

NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Felte & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Computer Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII, WordPerfect 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/917.410
FILING DATE: 26-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/578,953
FILING DATE: <Unknown>
APPLICATION NUMBER: EP 95 114 969.9
FILING DATE: 19-Sep-95

ATTORNEY/AGENT INFORMATION:
NAME: Hanson, NO. US20020098183A1man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: BOER 1059-PFF/NDH/SLH
TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 688-9200
 TELEFAX: (212) 838-3884
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 448 amino acid residues
 TYPE: amino acid
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 6:
 US-09-917-410-6

Query Match 100.0%; Score 2389; DB 9; Length 448;
 Best Local Similarity 100.0%; Pred. No. 8,3e-161;
 Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 QVQLVQSGAEVKKPESSTSVKQSCAKSGYFTSYVMHWVQAPGQGLEWIGYIPYNDGKY 60
DB 1 QVQLVQSGAEVKKPESSTSVKQSCAKSGYFTSYVMHWVQAPGQGLEWIGYIPYNDGKY 60
QY 61 NEKFKGRVITTSDESTNTAYMELSLRSEDTAVYYCAREEYGNVYRFDVWGQGLTVVS 120
DB 61 NEKFKGRVITTSDESTNTAYMELSLRSEDTAVYYCAREEYGNVYRFDVWGQGLTVVS 120
QY 121 SASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 180
DB 121 SASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 180
QY 181 SGLYSLSVVTVPSSSLGTQITTCNVDRHPSNTKYDKRVESEKGPCCSPAPEFLGSPS 240
DB 181 SGLYSLSVVTVPSSSLGTQITTCNVDRHPSNTKYDKRVESEKGPCCSPAPEFLGSPS 240
QY 241 VFLEPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFMNYYVDGVEVHNAKTKRREQFNST 300
DB 241 VFLEPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFMNYYVDGVEVHNAKTKRREQFNST 300
QY 301 YRVSVLTVLHODWLNQGEYKCKVSNKGLPSSIEKTIISKAKGPPEPQVYTLPPSQEEMT 360
DB 301 YRVSVLTVLHODWLNQGEYKCKVSNKGLPSSIEKTIISKAKGPPEPQVYTLPPSQEEMT 360
QY 361 KQVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTTPVLDSDGSFYLISRLTVDSRWOE 420
DB 361 KQVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTTPVLDSDGSFYLISRLTVDSRWOE 420
QY 421 GNVSFCSVMHEALHNHYTOKSLSLGK 448
DB 421 GNVSFCSVMHEALHNHYTOKSLSLGK 448

```

RESULT 2 US-10-428-408A-30

Sequence 30, Application US/10428408A
 Publication No. US20030235869A1
 GENERAL INFORMATION:
 APPLICANT: Celltech R&D Limited
 TITLE OF INVENTION: BIOLOGICAL PRODUCTS
 FILE REFERENCE: CARP0004-100
 CURRENT APPLICATION NUMBER: US/10/428,408A
 CURRENT FILING DATE: 2003-05-02
 NUMBER OF SEQ ID NOS: 51
 SOFTWARE: SeqMan9, version 1.02
 SEQ ID NO 30
 LENGTH: 467
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 NAME/KEY: CHAIN
 OTHER INFORMATION: Full sequence of grafted heavy chain
 US-10-428-408A-30

Query Match 93.2%; Score 2226; DB 12; Length 467;
 Best Local Similarity 93.5%; Pred. No. 2,9e-149;
 Matches 419; Conservative 10; Mismatches 19; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKPESSTSVKQSCAKSGYFTSYVMHWVQAPGQGLEWIGYIPYNDGKY 60

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DB 20 EVQLVQSGAEVKKPESSTSVKQSCAKSGYFTSYVMHWVQAPGQGLEWIGINGNVATY 79
QY 61 NEKFKGRVITTSDESTNTAYMELSLRSEDTAVYYCAREEYGNVYRFDVWGQGLTVVS 120
DB 80 RRFQGRVITTSDESTNTAYMELSLRSEDTAVYYCAREEYGNVYRFDVWGQGLTVVS 129
QY 121 SASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 180
DB 140 SASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 199
QY 181 SGLYSLSVVTVPSSSLGTQITTCNVDRHPSNTKYDKRVESEKGPCCSPAPEFLGSPS 240
DB 200 SGLYSLSVVTVPSSSLGTQITTCNVDRHPSNTKYDKRVESEKGPCCSPAPEFLGSPS 259
QY 241 VFLEPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFMNYYVDGVEVHNAKTKRREQFNST 300
DB 260 VFLEPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFMNYYVDGVEVHNAKTKRREQFNST 319
QY 301 YRVSVLTVLHODWLNQGEYKCKVSNKGLPSSIEKTIISKAKGPPEPQVYTLPPSQEEMT 360
DB 320 YRVSVLTVLHODWLNQGEYKCKVSNKGLPSSIEKTIISKAKGPPEPQVYTLPPSQEEMT 379
QY 361 KQVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTTPVLDSDGSFYLISRLTVDSRWOE 420
DB 380 KQVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTTPVLDSDGSFYLISRLTVDSRWOE 439
QY 421 GNVSFCSVMHEALHNHYTOKSLSLGK 448
DB 440 GNVSFCSVMHEALHNHYTOKSLSLGK 467

```

RESULT 3 US-10-401-344-2

Sequence 2, Application US/10401344
 Publication No. US20030194404A1
 GENERAL INFORMATION:
 APPLICANT: Schering Corporation and Abgenix, Inc.
 APPLICANT: Corvax, Jose
 TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO INTERLEUKIN-5 AND METHODS AND CO
 FILE REFERENCE: L101564W1
 CURRENT APPLICATION NUMBER: US/10/401,344
 CURRENT FILING DATE: 2003-03-27
 NUMBER OF SEQ ID NOS: 22
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 2
 LENGTH: 465
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: SIGNAL
 LOCATION: (1)..(19)
 OTHER INFORMATION:
 FEATURE:
 NAME/KEY: Variable Region
 LOCATION: (20)..(138)
 OTHER INFORMATION:
 FEATURE:
 NAME/KEY: CH1 Region
 LOCATION: (139)..(236)
 OTHER INFORMATION:
 FEATURE:
 NAME/KEY: Hinge Region
 LOCATION: (237)..(248)
 OTHER INFORMATION:
 FEATURE:
 NAME/KEY: CH2 Region
 LOCATION: (249)..(358)
 OTHER INFORMATION:
 FEATURE:
 NAME/KEY: CH3 Region

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/578,953
FILING DATE: 27-Dec-95
APPLICATION NUMBER: EP 95 112 895.8
FILING DATE: 17-Aug-95
APPLICATION NUMBER: EP 95 114 969.9
FILING DATE: 19-Sep-95
ATTORNEY/AGENT INFORMATION:
NAME: Norman D. Hanson
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: BOER 1059-PCT-PFF/NDH
TELEPHONE: (212) 688-9200
TELEFAX: (212) 688-9200
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 443
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-13152-4

Query Match 88.2%; Score 2106.5; DB 5; Length 443;
Best Local Similarity 88.4%; Pred. No. 1.9e-161;
Matches 396; Conservative 21; Mismatches 26; Indels 5; Gaps 2;

1 QVQLVDSGAEVKKGGSSVKVSCKASGYTFSTSYMMHWVRQAPGQGLEWIGYIYPNDQTKY 60
1 EVQLVESGGGLVQGGSLRLSCAASGFTFSTYAMSWVRQAPGKLEWVAST-STGSGSTYY 59
61 NEKFKGRVITTSDESTNTAYMELSLRSEDTAVYYCAREEYGVYRFDVWGQGLTVTVS 120
60 PDSYKGRFTISRDNAKNTLYIQMNSLAIEDTAVYYCARD---YDGFYDWGQGLTVTVS 115
121 SASTKGPSVPLAPCSRSTSESTALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 180
116 SASTKGPSVPLAPCSRSTSESTALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 175
181 SGLYSLSVTVVSSSLGTCTYTCNVDHKPSNTKVDKRVESKYPPEPSCPAPPEFLG 240
176 SGLYSLSVTVVSSSLGTCTYTCNVDHKPSNTKVDKRVESKYPPEPSCPAPPEFLG 235
241 VFLEPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFMWYDGEVHNAAKTKPREEQNST 300
236 VFLEPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFMWYDGEVHNAAKTKPREEQNST 295
301 YRVVSVLTVLHODWLNKEKCYKSNKGLPSISIKTSKAKGQPREPQVYTLPPSQEEMT 360
296 YRVVSVLTVLHODWLNKEKCYKSNKGLPSISIKTSKAKGQPREPQVYTLPPSQEEMT 355
361 KNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFLYSRLTYDKSR 420
356 KNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFLYSRLTYDKSR 415
421 GNVFSCSVMEHALHNHYTKSLSLGK 448
416 GNVFSCSVMEHALHNHYTKSLSLGK 443

RESULT 4
US-08-458-516-13
Sequence 13, Application US/08458516
Patent No. 577085
GENERAL INFORMATION:
APPLICANT: Co, Man Sung
APPLICANT: Tso, J. Yun
TITLE OF INVENTION: Humanized Antibodies Reactive with
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:

ADDRESSEE: William M. Smith
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,516
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/059,159
FILING DATE: 03-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-37-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 449 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-458-516-13

Query Match 88.0%; Score 2101.5; DB 1; Length 449;
Best Local Similarity 88.7%; Pred. No. 4.9e-161;
Matches 400; Conservative 20; Mismatches 26; Indels 5; Gaps 3;

1 QVQLVDSGAEVKKGGSSVKVSCKASGYTFSTSYMMHWVRQAPGQGLEWIGYIYPNDQTKY 60
1 QVQLVDSGAEVKKGGSSVKVSCASGYAFNTLYIEHWVRQAPGQGLEWIGYIYGGSGTNY 60
61 NEKFKGRVITTSDESTNTAYMELSLRSEDTAVYYCAREEYGVYRFDVWGQGLTVTVS 120
60 PDSYKGRFTISRDNAKNTLYIQMNSLAIEDTAVYYCARD-GNY-GWFAVWGQGLTVTVS 118
121 SASTKGPSVPLAPCSRSTSESTALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 180
119 SASTKGPSVPLAPCSRSTSESTALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 178
181 SGLYSLSVTVVSSSLGTCTYTCNVDHKPSNTKVDKRVESK---YGPPEPSCPAPPEFLG 237
179 SGLYSLSVTVVSSSLGTCTYTCNVNHKPSNTKVDKRVESKCDKTHCTPPAPPEFLG 238
238 GPGVFLPEPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFMWYDGEVHNAAKTKPREEQ 297
239 GPGVFLPEPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFMWYDGEVHNAAKTKPREEQ 298
298 NSTYRVVSVLTVLHODWLNKEKCYKSNKGLPSISIKTSKAKGQPREPQVYTLPPSQE 357
299 NSTYRVVSVLTVLHODWLNKEKCYKSNKGLPSISIKTSKAKGQPREPQVYTLPPSRD 358
358 EMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFLYSRLTYDKSR 417
359 EMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFLYSRLTYDKSR 418
418 WQGNVFSCSVMEHALHNHYTKSLSLGK 448
419 WQGNVFSCSVMEHALHNHYTKSLSLGK 449

RESULT 5
US-09-027-449-71

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; Sequence 71, Application US/09027449
; Patent No. 6025158
; GENERAL INFORMATION:
; APPLICANT: Gonzalez, Tania R.
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/027,449
; FILING DATE: 20-Feb-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/074,330
; FILING DATE: 22-Jan-1998
; APPLICATION NUMBER: 60/038,664
; FILING DATE: 21-Feb-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R3-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-09-027-449-71

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```

Query Match      85.1%; Score 2033; DB 3; Length 452;
Best Local Similarity 84.1%; Pred. No. 1.6e-155;
Matches 382; Conservative 33; Mismatches 31; Indels 8; Gaps 3;

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```

QY 1 QVQLVQSGAEVKKPKSSSKVSKCSAGYFTSYVMHWVRQAPGQGLEWIGYIYPNDGTY 60
DB 1 EVQLVQSGGGLVQPGGSLRLSCAASGYFSSHYMHMVRQAPGKGLIEWGYIDPSNGETTY 60
QY 61 NEKFKRVTITSDSTNTAYMELSLRSEDYAVYYCAREEY---GNYRYFEDWOGTLY 117
DB 61 NQKFKRFTLSRSDNSKNTAYLQNMNLSLRADYAVYYCARDDYRNGDM--FEDWOGGTLV 118
QY 118 TVSSASTGSPVFPPLAPCSRSTSESTAALGCLVQDYFPEPTVTSWNSGALTSGVHTFPAY 177
DB 119 TVSSASTGSPVFPPLAPSSKSTSGTAAIGCLVKDYFPEPTVTSWNSGALTSGVHTFPAY 178
QY 178 LQSSGLYSLSSVYTPSSSLGTYTTCNVDPKPSNTKVDKRVESK---YGPPECSCPAPE 234
DB 179 LQSSGLYSLSSVYTPVSSSLGTYTTCNVNPKPSNTKVDKRVESKCDTHCPCPAPE 238
QY 235 FLGGPSVFLPPPKPDITMISRTPEYTCVVVDVQSDPEVQFNWYVDGVEVNAKTKPRE 294
DB 239 ILGGPSVFLPPPKPDITMISRTPEYTCVVVDVSHEDPEVKFNWYVDGVEVNAKTKPRE 298
QY 295 EQFNSTYRVAVSVLTVLHDMNLNGKEYKCVSNKALPLPFIETISKAKGQPREPQVYTLPP 354
DB 299 EQFNSTYRVAVSVLTVLHDMNLNGKEYKCVSNKALPLPFIETISKAKGQPREPQVYTLPP 358

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QY 355 SQEEMTNQVSLTCLVKGFIIPSDIAVWESNGQEPNNYKTTTPVLDSDGSFLYSRLTVD 414
DB 359 SREEMTNQVSLTCLVKGFIIPSDIAVWESNGQEPNNYKTTTPVLDSDGSFLYSRLTVD 418
QY 415 KSRWQGNVFSQSVMEALNHYTQKSLSLGK 448
DB 419 KSRWQGNVFSQSVMEALNHYTQKSLSLSPK 452

```

RESULT 6

```

US-09-026-985-71
; Sequence 71, Application US/09026985
; Patent No. 6133426
; GENERAL INFORMATION:
; APPLICANT: Gonzalez, Tania R.
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/026,985
; FILING DATE: 20-Feb-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R3-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-09-026-985-71

```

```

Query Match      85.1%; Score 2033; DB 3; Length 452;
Best Local Similarity 84.1%; Pred. No. 1.6e-155;
Matches 382; Conservative 33; Mismatches 31; Indels 8; Gaps 3;

```

```

QY 1 QVQLVQSGAEVKKPKSSSKVSKCSAGYFTSYVMHWVRQAPGQGLEWIGYIYPNDGTY 60
DB 1 EVQLVQSGGGLVQPGGSLRLSCAASGYFSSHYMHMVRQAPGKGLIEWGYIDPSNGETTY 60
QY 61 NEKFKRVTITSDSTNTAYMELSLRSEDYAVYYCAREEY---GNYRYFEDWOGTLY 117
DB 61 NQKFKRFTLSRSDNSKNTAYLQNMNLSLRADYAVYYCARDDYRNGDM--FEDWOGGTLV 118
QY 118 TVSSASTGSPVFPPLAPCSRSTSESTAALGCLVQDYFPEPTVTSWNSGALTSGVHTFPAY 177
DB 119 TVSSASTGSPVFPPLAPSSKSTSGTAAIGCLVKDYFPEPTVTSWNSGALTSGVHTFPAY 178
QY 178 LQSSGLYSLSSVYTPSSSLGTYTTCNVDPKPSNTKVDKRVESK---YGPPECSCPAPE 234
DB 179 LQSSGLYSLSSVYTPVSSSLGTYTTCNVNPKPSNTKVDKRVESKCDTHCPCPAPE 238
QY 235 FLGGPSVFLPPPKPDITMISRTPEYTCVVVDVQSDPEVQFNWYVDGVEVNAKTKPRE 294
DB 239 ILGGPSVFLPPPKPDITMISRTPEYTCVVVDVSHEDPEVKFNWYVDGVEVNAKTKPRE 298

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QY 295 EGFNSTRYVSVLTVLHODMLNGKEYCKYSNKGLPSSIEKTIKSKAGQPREPOVYTLTP 354
Db 299 EQVNSTRYVSVLTVLHODMLNGKEYCKYSNKGLPAPIEKTIKSKAGQPREPOVYTLTP 358
QY 355 SOEEMTKNOVSLTCLVKGFPSPDIAVWESNGQPENNYKTPPVLDSDGSFFLYSKLTV 414
Db 359 SREEMTKNOVSLTCLVKGFPSPDIAVWESNGQPENNYKTPPVLDSDGSFFLYSKLTV 418
QY 415 KSRWQGNVFSQSVMEALHNYTKSLSLGK 448
Db 419 KSRWQGNVFSQSVMEALHNYTKSLSLGK 452

RESULT 7
US-09-121-952A-71
Sequence 71, Application US/09121952A
Patent No. 6458355
GENERAL INFORMATION:
APPLICANT: Genentech, Inc., Hsei, Vanessa
APPLICANT: Koumenis, Iphigenia
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
APPLICANT: Shahrokh, Zahra
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONUGATES
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/121,952A
FILING DATE: 24-Jul-1998
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/074330
FILING DATE: 22-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/075467
FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 452 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-121-952A-71

Query Match 85.1%; Score 2033; DB 4: Length 452;
Best Local Similarity 84.1%; Pred. No. 1.6e-155;
Matches 382; Conservative 33; Mismatches 31; Indels 8; Gaps 3;

QY 1 QVQLVQSGAEVKKPGSSVKASGYSYFTSYVMHWVQADGQGLEWIGYIYPYNDGTRY 60
Db 1 EVQLVQSGGGLVQPGSGSLRCAASGYISFSSHYMHMWVQAQKGLIEWGIIYDPSNGETTY 60
QY 61 NEKFKGRVTTISDESTNTATYMLSLRSEDTAVVYICAREEY--GNVRYRFDVWGQGLTV 117

Db 61 NQKFKGRFTLSRDNSKNTATYALQWMSLRAEDTAVYICARGDYRNGDW--FFDVWGQGLTV 118
QY 118 TVSSASTKGPSPVEPLACSRSTSESTALGLVADYEPPEVYTSWNSGALTSGVHTPPAV 177
Db 119 TVSSASTKGPSPVEPLAASSKSTSGTALACGLVADYEPPEVYTSWNSGALTSGVHTPPAV 178
QY 178 LQSSGLYSLSVSVTPSSSLGTQYICNVNHNKPSNTKVDKVEKSCDKHTTCCPAPAE 234
Db 179 LQSSGLYSLSVSVTPSSSLGTQYICNVNHNKPSNTKVDKVEKSCDKHTTCCPAPAE 238
QY 235 FLGGPSVFLPPPKDLMISRTPEVTCVAVDSQDEPVOFMNVYGVGVHNAKTPRE 294
Db 239 FLGGPSVFLPPPKDLMISRTPEVTCVAVDSQDEPVEKFNMYVGVGVHNAKTPRE 298
QY 295 EGFNSTRYVSVLTVLHODMLNGKEYCKYSNKGLPSSIEKTIKSKAGQPREPOVYTLTP 354
Db 299 EQVNSTRYVSVLTVLHODMLNGKEYCKYSNKGLPAPIEKTIKSKAGQPREPOVYTLTP 358
QY 355 SOEEMTKNOVSLTCLVKGFPSPDIAVWESNGQPENNYKTPPVLDSDGSFFLYSKLTV 414
Db 359 SREEMTKNOVSLTCLVKGFPSPDIAVWESNGQPENNYKTPPVLDSDGSFFLYSKLTV 418
QY 415 KSRWQGNVFSQSVMEALHNYTKSLSLGK 448
Db 419 KSRWQGNVFSQSVMEALHNYTKSLSLGK 452

RESULT 8
US-09-234-340A-71
Sequence 71, Application US/09234340A
Patent No. 6468532
GENERAL INFORMATION:
APPLICANT: Genentech, Inc., Hsei, Vanessa
APPLICANT: Koumenis, Iphigenia
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
APPLICANT: Shahrokh, Zahra
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONUGATES
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,340A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/121,952
FILING DATE: 24-Jul-1998
APPLICATION NUMBER: 60/074330
FILING DATE: 22-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/075467
FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 71:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 452 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-09-234-340A-71

Query Match 85.1%; Score 2033; DB 4; Length 452;
 Best Local Similarity 84.1%; Pred. No. 1,6e-155;
 Matches 382; Conservative 33; Mismatches 31; Indels 8; Gaps 3;

QY 1 QVQLVQSGAEVKKPKSSSKAKVSCAKAGYFTSTVMMHWVROAPGGGLEWIGIYIPNDGK 60
 DB 1 EVQLVQSGGGLVQPGSGLRSLSCAASGYSFSSHYMMHWVROAPGKLEWVGVIDPSNGETTY 60
 QY 61 NEKFKGRVITTSDESTNTAYMELSLRSEDTAVYVCAREEY---GNVYRFPDWGQGLTV 117
 DB 61 NQKFKGRFTLSRDNSKNTAIYLOMNSLRADETAVYVCARGDVRINDW--FEDVWGQGLTV 118
 QY 118 TVSSASTKGPVFPPLAPCSRSTSESTALGCLVKDYFPEPVTVSNMGSALTSGVHTFPAV 177
 DB 119 TVSSASTKGPVFPPLAPSKSTSGTAAIGCLVKDYFPEPVTVSNMGSALTSGVHTFPAV 178
 QY 178 LQSSGLYSLSVTVTPSSSLGRTKTYTCNVDRHPSNTKYDKVESK---YGPCCPCPAPE 234
 DB 179 LQSSGLYSLSVTVTPSSSLGRTQTYICNVNHRPSNTKYDKVEPKSCDRTHTCCPCPAPE 238
 QY 235 FLGPGSVFLFPKPKDITLMSRTPEVTCVVDVDSQEDPEVQFMWYVDGVEVNAKTKPRE 294
 DB 239 LLGGSVFLFPKPKDITLMSRTPEVTCVVDVSHEDPEVKRWYVDGVEVNAKTKPRE 298
 QY 295 EQFNSTYRVSVLTVLHODMLNGKEYCKVSNKGLPSSIEKTISSAKGQPREPQVYTLPP 354
 DB 299 EQYNSTYRVSVLTVLHODMLNGKEYCKVSNKGLPAPIEKTISSAKGQPREPQVYTLPP 358
 QY 355 SEENTKQVSLTCLVKGFPSPDIAVEMWNSQPENNYKTPPVLDSDGSFFLYSLRYVD 414
 DB 359 SEENTKQVSLTCLVKGFPSPDIAVEMWNSQPENNYKTPPVLDSDGSFFLYSLRYVD 418
 QY 415 KSRMOGNVFCSCVMHEALHNHYTQKSLSLCK 448
 DB 419 KSRMOGNVFCSCVMHEALHNHYTQKSLSLCK 452

RESULT 9
 US-08-523-894-8
 Sequence 8, Application US/08523894
 Patent No. 6136310

GENERAL INFORMATION:
 APPLICANT: Hanna, Nabil
 APPLICANT: Newman, Roland A.
 APPLICANT: Reff, Mitchell E.
 TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
 TITLE OF INVENTION: Therapy
 NUMBER OF SEQUENCES: 59
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
 STREET: 699 Prince Street
 CITY: Alexandria
 STATE: VA
 COUNTRY: USA
 ZIP: 22314-3187
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/523,894
 FILING DATE: 06-SEP-1995
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Teskin, Robin L.

REGISTRATION NUMBER: 35,030
 REFERENCE/DOCKET NUMBER: 012712-165
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-836-6620
 TELEFAX: 703-836-2021
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 467 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-523-894-8

Query Match 84.8%; Score 2026; DB 3; Length 467;
 Best Local Similarity 85.5%; Pred. No. 6.1e-155;
 Matches 384; Conservative 19; Mismatches 44; Indels 2; Gaps 2;

QY 1 QVQLVQSGAEVKKRQSSKAKVSCAKAGYFTT-SYMMHWVROAPGGGLEWIGIYIPNDGK 59
 DB 20 QVQLVQSGPGLVKPESTLSTCVSGSISGDYVFWIRQSPGKLEWIGIYVSGGGIN 79
 QY 60 YNEKFKGRVITTSDESTNTAYMELSLRSEDTAVYVCAREEYGVYRFPDWGQGLTV 119
 DB 80 YNPGLNRRVSIIDTSKTLFSLKRSVTAADTAVYCA-SMLKYLHMLYMGQGLTV 138
 QY 120 SSASTKGPVFPPLAPCSRSTSESTALGCLVKDYFPEPVTVSNMGSALTSGVHTFPAV 179
 DB 139 SSASTKGPVFPPLAPCSRSTSESTALGCLVKDYFPEPVTVSNMGSALTSGVHTFPAV 198
 QY 180 SSGLYSLSVTVTPSSSLGRTKTYTCNVDRHPSNTKYDKRVSKYGPCCPCPAPEFLG 239
 DB 199 SSGLYSLSVTVTPSSSLGRTTYTCNVDRHPSNTKYDKRVSKYGPCCPCPAPEFLG 258
 QY 240 SVFLFPKPKDITLMSRTPEVTCVVDVDSQEDPEVQFMWYVDGVEVNAKTKPREEQNS 299
 DB 259 SVFLFPKPKDITLMSRTPEVTCVVDVDSQEDPEVQFMWYVDGVEVNAKTKPREEQNS 318
 QY 300 TYRVSVLTVLHODMLNGKEYCKVSNKGLPSSIEKTISSAKGQPREPQVYTLPPSQEEM 359
 DB 319 TYRVSVLTVLHODMLNGKEYCKVSNKGLPSSIEKTISSAKGQPREPQVYTLPPSQEEM 378
 QY 360 TKQVSLTCLVKGFPSPDIAVEMWNSQPENNYKTPPVLDSDGSFFLYSLRYVDKSNQ 419
 DB 379 TKQVSLTCLVKGFPSPDIAVEMWNSQPENNYKTPPVLDSDGSFFLYSLRYVDKSNQ 438
 QY 420 EGNVFCSCVMHEALHNHYTQKSLSLCK 448
 DB 439 EGNVFCSCVMHEALHNHYTQKSLSLCK 467

RESULT 10
 US-09-301-593-43
 Sequence 43, Application US/09301593A
 Patent No. 6455677

GENERAL INFORMATION:
 APPLICANT: Park, John E.
 APPLICANT: Garin-Chesa, Pilar
 APPLICANT: Bamberger, Uwe
 APPLICANT: Leger, Olivier
 APPLICANT: Saldanha, Jose W.
 APPLICANT: Rectig, Wolfgang J.
 TITLE OF INVENTION: FAP-specific Antibody with Improved Productibility
 FILE REFERENCE: 0652.1890001
 CURRENT APPLICATION NUMBER: US/09/301,593A
 EARLIER FILING DATE: 1999-04-29
 EARLIER APPLICATION NUMBER: EP 98107925.4
 EARLIER FILING DATE: 1998-04-30
 EARLIER APPLICATION NUMBER: US 60/086,049
 EARLIER FILING DATE: 1998-05-18
 NUMBER OF SEQ ID NOS: 108
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO 43
 LENGTH: 472

TYPE: PRT
ORGANISM: Homo sapiens
US-09-301-593-43

Query Match 84.7%; Score 2023.5; DB 4; Length 472;
Best Local Similarity 86.1%; Pred. No. 9.8e-155;
Matches 391; Conservative 17; Mismatches 39; Indels 7; Gaps 4;

QY 1 QVQLVQSGAEVKKPGSSVKVSCKASGVTFTSYVMHWRAQPGQGLEWIGYIYPNDGTRY 60
DB 20 QVQLVQSGAEVKKPGSSVKVSCKASGVTFTSYVMHWRAQPGQGLEWIGYIYPNDGTRY 79
QY 61 NEKRGRTITSDSTNAYMELSLRSEDYAVYCARAE--YGVNRYRDWVGQGLV 117
DB 80 NQKRGRTITLVGASASTAYMELSLRSEDYAVYCARRIAYGDEGHANDYVGQGLV 139
QY 118 TVSSASTKGPSEVFLAPCSRSTSESTALGCLVVDYFPEPTVSMNSGALTSVHTFPAY 177
DB 140 TVSS-STKGPSEVFLAPCSRSTSGGTALGCLVVDYFPEPTVSMNSGALTSVHTFPAY 198
QY 178 LQSSGLVSLSSVTVPPSSSLGTYTCNVDHKPSNTKYDKRVEK--YGPCCPCPAPE 234
DB 199 LQSSGLVSLSSVTVPPSSSLGTYTCNVNKHKPSNTKYDKVBPCKCDKHTCPCPAPE 258
QY 235 FLGSPSVFLPPPKKDTLMISRTEVTCVVDVSGQEDPEVQFNMYVDGVEVHNAKTKPRE 294
DB 259 LLGSPSVFLPPPKKDTLMISRTEVTCVVDVSHEDPEVKFNMYVDGVEVHNAKTKPRE 318
QY 295 EQFSTRYRVSVLTVLHODMLNGEKYCKVSNKGLPSIETKISKAGQPREPOVYTLPP 354
DB 319 EQVNSTRYRVSVLTVLHODMLNGEKYCKVSNKGLPAIEKTIKAKQPREPOVYTLPP 378
QY 355 SQEEMTKNQVSLTCLVKGFPYSDIAVEMESNGQPENNYKTPPYLDSGSEFVLSRLTVD 414
DB 379 SREEMTKNQVSLTCLVKGFPYSDIAVEMESNGQPENNYKTPPYLDSGSEFVLSKLTV 438
QY 415 KSRWQEGNVFSCSYMHEALHNHYTKSLSLSGK 448
DB 439 KSRWQEGNVFSCSYMHEALHNHYTKSLSLSPGK 472

RESULT 11

US-08-378-939-10
Sequence 10, Application US/08378939
Patent No. 5876961
GENERAL INFORMATION:
APPLICANT: CROME, JAMES SCOTT
APPLICANT: LEWIS, ALAN PETER
TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
STREET: 555 THIRTEENTH ST. N.W.
CITY: WASHINGTON
STATE: D. C.
COUNTRY: U.S.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,939
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/952640
FILING DATE: 01-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: ERNST, BARBARA G
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1808-118

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 783-6040

TELEFAX: (202) 783-6031

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 476 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-378-939-10
Query Match 84.7%; Score 2023.5; DB 2; Length 476;
Best Local Similarity 84.5%; Pred. No. 9.9e-155;
Matches 386; Conservative 29; Mismatches 33; Indels 9; Gaps 3;

QY 1 QVQLVQSGAEVKKPGSSVKVSCKASGVTFTSYVMHWRAQPGQGLEWIGYIYPNDGTRY 60
DB 20 QVQLVQSGAEVKKPGSSVKVSCKASGVTFTSYVMHWRAQPGQGLEWIGYIYPNDGTRY 79
QY 61 NEKRGRTITSDSTNAYMELSLRSEDYAVYCARAE--YGVNRYRDWVGQGLV 114
DB 80 NQKRGRTITLVGASASTAYMELSLRSEDYAVYCATDRYRQANFRRARVGMFDPWGQGL 139
QY 115 TVSSASTKGPSEVFLAPCSRSTSESTALGCLVVDYFPEPTVSMNSGALTSVHTFPAY 174
DB 140 TVSSASTKGPSEVFLAPCSRSTSGGTALGCLVVDYFPEPTVSMNSGALTSVHTFPAY 199
QY 175 PAVLQSSGLVSLSSVTVPPSSSLGTYTCNVDHKPSNTKYDKRVEK--YGPCCPCPCP 231
DB 200 PAVLQSSGLVSLSSVTVPPSSSLGTYTCNVNKHKPSNTKYDKRVEKSCDKHTCPCP 259
QY 232 APEFLGSPSVFLPPPKKDTLMISRTEVTCVVDVSGQEDPEVQFNMYVDGVEVHNAKTK 291
DB 260 APEFLGSPSVFLPPPKKDTLMISRTEVTCVVDVSHEDPEVKFNMYVDGVEVHNAKTK 319
QY 292 PREQFSTRYRVSVLTVLHODMLNGEKYCKVSNKGLPSIETKISKAGQPREPOVYTL 351
DB 320 PREQVNSTRYRVSVLTVLHODMLNGEKYCKVSNKGLPAIEKTIKAKQPREPOVYTL 379
QY 352 LPPEQEMTKNQVSLTCLVKGFPYSDIAVEMESNGQPENNYKTPPYLDSGSEFVLSRL 411
DB 380 LPPEQEMTKNQVSLTCLVKGFPYSDIAVEMESNGQPENNYKTPPYLDSGSEFVLSKL 439
QY 412 TVDKSRWQEGNVFSCSYMHEALHNHYTKSLSLSGK 448
DB 440 TVDKSRWQEGNVFSCSYMHEALHNHYTKSLSLSPGK 476

RESULT 12

US-08-788-800-12
Sequence 12, Application US/08788800
Patent No. 5914112
GENERAL INFORMATION:
APPLICANT: Bednar, Martin M.
APPLICANT: Thomas, G. Roger
TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/788,800
FILING DATE: 22-Jan-1997

```

CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0987r1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 450 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-788-800-12

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```

Query Match      84.6%; Score 2022; DB 2; Length 450;
Best Local Similarity 84.0%; Pred. No. 1.2e-154;
Matches 379; Conservative 31; Mismatches 37; Indels 4; Gaps 2;

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QY 1 QVQLVQSGAEVKKPGSSVKVSCKAASGTTFTSYVMHWRAQPGQGLEWIGYIYPNDGTKY 60
DB 1 EVQLVESGGGLVQPGSGRLSCATISGTYFTETMHMMRAQPGKLEWVAGINPKNGTSH 60
QY 61 NEKFKGRTITSDSTNTAYNELSLRSEDTAVYYCAR--EEYGNVYRFYDVGQGTLLV 117
DB 61 NORFMDRFTISVDKSTSTAYQMNSLRADFAVYYCAWRGGLNYGFDVRFYDVGQGTLLV 120
QY 118 TVSSASTKGPVFLAPCSRSTSESTALGCLVKDYFPEPVVSWNSGALTSGVHTFPAV 177
DB 121 TVSSASTKGPVFLAPCSRSTSESTALGCLVKDYFPEPVVSWNSGALTSGVHTFPAV 180
QY 178 LOSGLYSLSSVVTVPSSSLGKTTCNVVDHKPSTKVDKRVESKYGPCCSPAPFLIG 237
DB 181 LOSGLYSLSSVVTVPSSSLGKTTCNVVDHKPSTKVDKRVESKYGPCCSPAPFLIG 239
QY 238 GPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVOFNNWYDGMVHNATKPREQF 297
DB 240 GPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVOFNNWYDGMVHNATKPREQF 299
QY 298 NSTYRVSVLTVLHQMVLNGEKYKVSNNKGLPSIETKISKAKQPREPQVYTLPPSQE 357
DB 300 NSTFRVSVLTVLHQMVLNGEKYKVSNNKGLPSIETKISKAKQPREPQVYTLPPSQE 359
QY 358 EMTKNQVSLTCLVKGFPSPDIAYVESNGQPENNYKTTTPVLDSDGSFFLYSLRLTVDSKR 417
DB 360 EMTKNQVSLTCLVKGFPSPDIAYVESNGQPENNYKTTTPVLDSDGSFFLYSLRLTVDSKR 419
QY 418 WQGNVFCSCVMHEALHNHYTQKSLSLSPGK 448
DB 420 WQGNVFCSCVMHEALHNHYTQKSLSLSPGK 450

```

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RESULT 13
US-07-934-373C-23
Sequence 23, Application US/07934373C
Patent No. 5821337
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

```

```

SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934.373C
FILING DATE: 21-Aug-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 469 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-07-934-373C-23

```

```

Query Match      84.6%; Score 2022; DB 2; Length 469;
Best Local Similarity 84.0%; Pred. No. 1.3e-154;
Matches 379; Conservative 31; Mismatches 37; Indels 4; Gaps 2;

```

```

QY 1 QVQLVQSGAEVKKPGSSVKVSCKAASGTTFTSYVMHWRAQPGQGLEWIGYIYPNDGTKY 60
DB 20 EVQLVESGGGLVQPGSGRLSCATISGTYFTETMHMMRAQPGKLEWVAGINPKNGTSH 79
QY 61 NEKFKGRTITSDSTNTAYNELSLRSEDTAVYYCAR--EEYGNVYRFYDVGQGTLLV 117
DB 80 NORFMDRFTISVDKSTSTAYQMNSLRADFAVYYCAWRGGLNYGFDVRFYDVGQGTLLV 139
QY 118 TVSSASTKGPVFLAPCSRSTSESTALGCLVKDYFPEPVVSWNSGALTSGVHTFPAV 177
DB 140 TVSSASTKGPVFLAPCSRSTSESTALGCLVKDYFPEPVVSWNSGALTSGVHTFPAV 199
QY 178 LOSGLYSLSSVVTVPSSSLGKTTCNVVDHKPSTKVDKRVESKYGPCCSPAPFLIG 237
DB 181 LOSGLYSLSSVVTVPSSSLGKTTCNVVDHKPSTKVDKRVESKYGPCCSPAPFLIG 239
QY 238 GPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVOFNNWYDGMVHNATKPREQF 297
DB 259 GPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVOFNNWYDGMVHNATKPREQF 318
QY 298 NSTYRVSVLTVLHQMVLNGEKYKVSNNKGLPSIETKISKAKQPREPQVYTLPPSQE 357
DB 319 NSTFRVSVLTVLHQMVLNGEKYKVSNNKGLPSIETKISKAKQPREPQVYTLPPSQE 378
QY 358 EMTKNQVSLTCLVKGFPSPDIAYVESNGQPENNYKTTTPVLDSDGSFFLYSLRLTVDSKR 417
DB 379 EMTKNQVSLTCLVKGFPSPDIAYVESNGQPENNYKTTTPVLDSDGSFFLYSLRLTVDSKR 438
QY 418 WQGNVFCSCVMHEALHNHYTQKSLSLSPGK 448
DB 439 WQGNVFCSCVMHEALHNHYTQKSLSLSPGK 469

```

```

RESULT 14
US-08-437-642B-23
Sequence 23, Application US/08437642B
Patent No. 6054297
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.

```

STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437, 642B
FILING DATE: 09-May-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 469 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-437-642B-23

Query Match 84.6%; Score 2022; DB 3; Length 469;
Best Local Similarity 84.0%; Pred. No. 1.3e-154;
Matches 379; Conservative 31; Mismatches 37; Indels 4; Gaps 2;
QY 1 QVQLVQSGAEVKKPGSSVKVCCKASGYTFTSYVMHWRAQPGGLEWIGYIYPNDGTKY 60
20 EVQLVESGGGLVQGGSLRLSCATSGYTFETYMHWMMRQAGKGLEWVAGINPNKGTS 79
QY 61 NEKRGKVTITSDSTNTAYMELSLRSEDTAVYYCAR--EEYGNVYRYFDWVGQGLTV 117
80 NORFMDFTISVDKSTSTAYVMQNSLRADTAIVYYCARMRGLNPGFVRYFDWVGQGLTV 139
Db 118 TVSSASTKGPSVFLAPCSRSTSESTALGCLVVDYPEPEVTVMSNGALTSVHTTPAV 177
140 TVSSASTKGPSVFLAPCSRSTSESTALGCLVVDYPEPEVTVMSNGALTSVHTTPAV 199
QY 178 LOSGGLYSLSSVTVTPSSSLGTRKYTCNVDRKPSNTKVDKVESKYGPPCPSPCAPRFLG 237
200 LOSGGLYSLSSVTVTPSSSLGTRKYTCNVDRKPSNTKVDKVESKYGPPCPSPCAPR-VA 258
Db 238 GPSVFLPPEPKKDTLMISRTPEVTCVVDVDSQEDPEVQFMWYVDGVEVHNAKTKPREEO 297
259 GPSVFLPPEPKKDTLMISRTPEVTCVVDVDSQEDPEVQFMWYVDGVEVHNAKTKPREEO 318
QY 298 NSTFRVSVLTVLVHODMLNGEKYCKVSNKGLPSIEKTIISKAGOPREPQVYTLPSR 357
319 NSTFRVSVLTVLVHODMLNGEKYCKVSNKGLPSIEKTIISKAGOPREPQVYTLPSR 378
Db 358 EMTNQVSLTCLVNGFYPSDIAVEMESNGOPENNYKTPPVLDSDGSEFFLYSRLTVDKSR 417
379 EMTNQVSLTCLVNGFYPSDIAVEMESNGOPENNYKTPPVLDSDGSEFFLYSRLTVDKSR 438
QY 418 WQGNVFSGSVMHAEALHNHTYQKSLSLSLGK 448

RESULT 15
US-08-146-206C-23
Sequence 23. Application US/08146206C
Patent No. 6407213
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146,206C
FILING DATE: 17-No. 6407213-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 469 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-146-206C-23

Query Match 84.6%; Score 2022; DB 4; Length 469;
Best Local Similarity 84.0%; Pred. No. 1.3e-154;
Matches 379; Conservative 31; Mismatches 37; Indels 4; Gaps 2;
QY 1 QVQLVQSGAEVKKPGSSVKVCCKASGYTFTSYVMHWRAQPGGLEWIGYIYPNDGTKY 60
20 EVQLVESGGGLVQGGSLRLSCATSGYTFETYMHWMMRQAGKGLEWVAGINPNKGTS 79
QY 61 NEKRGKVTITSDSTNTAYMELSLRSEDTAVYYCAR--EEYGNVYRYFDWVGQGLTV 117
80 NORFMDFTISVDKSTSTAYVMQNSLRADTAIVYYCARMRGLNPGFVRYFDWVGQGLTV 139
Db 118 TVSSASTKGPSVFLAPCSRSTSESTALGCLVVDYPEPEVTVMSNGALTSVHTTPAV 177
140 TVSSASTKGPSVFLAPCSRSTSESTALGCLVVDYPEPEVTVMSNGALTSVHTTPAV 199
QY 178 LOSGGLYSLSSVTVTPSSSLGTRKYTCNVDRKPSNTKVDKVESKYGPPCPSPCAPRFLG 237
200 LOSGGLYSLSSVTVTPSSSLGTRKYTCNVDRKPSNTKVDKVESKYGPPCPSPCAPR-VA 258
Db 238 GPSVFLPPEPKKDTLMISRTPEVTCVVDVDSQEDPEVQFMWYVDGVEVHNAKTKPREEO 297
259 GPSVFLPPEPKKDTLMISRTPEVTCVVDVDSQEDPEVQFMWYVDGVEVHNAKTKPREEO 318
QY 298 NSTFRVSVLTVLVHODMLNGEKYCKVSNKGLPSIEKTIISKAGOPREPQVYTLPSR 357
319 NSTFRVSVLTVLVHODMLNGEKYCKVSNKGLPSIEKTIISKAGOPREPQVYTLPSR 378

Oy 358 EMTKNQVSLTCLVKGFYPSDIAVEMESNGOPENNYKTTPVLDSDGSEFELYRLTVDKSR 417
Db 379 EMTKNQVSLTCLVKGFYPSDIAVEMESNGOPENNYKTTPMLDSDGSEFELYSKLTVDKSR 438
Oy 418 WQGNVFCSCSVWHEALHNHYTOKSLSLGK 448
Db 439 WQGNVFCSCSVWHEALHNHYTOKSLSLSPGK 469

Search completed: December 31, 2003, 10:33:11
Job time : 17.8548 secs